

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 14, 2005, 21:44:35 ; Search time 223 Seconds  
(without alignments)  
397.337 Million cell updates/sec

Title: US-10-614-990-2

Perfect score: 1268

Sequence: 1 MLQNSAVLLVLVISASATHE.....NLRGEEDSPSHIKRTSHESA 247

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_23Sep04:\*

1: geneseqp1980s:\*

2: geneseqp1990s:\*

3: geneseqp2000s:\*

4: geneseqp2001s:\*

5: geneseqp2002s:\*

6: geneseqp2003as:\*

7: geneseqp2003bs:\*

8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result No.	Score	Query			Description
		Match	Length	DB	
1	1268	100.0	247	2	AAR84522 Stannioca
2	1268	100.0	247	3	Aab23264 Human sta
3	1268	100.0	247	3	Aay55750 Human sta
4	1268	100.0	247	3	Aay57166 Human cor
5	1268	100.0	247	3	Aay92901 Human sta
6	1268	100.0	247	4	Aab62473 Human sta
7	1268	100.0	247	4	Aab62690 Lng108, a
8	1268	100.0	247	5	Abb06259 Human sta
9	1268	100.0	247	6	Abp97748 Amino aci

10	1268	100.0	247	6	ABR47600	Abr47600 Breast ca
11	1268	100.0	247	6	ABG72290	Abg72290 Human Cor
12	1268	100.0	247	7	ADD48082	Add48082 Human Pro
13	1268	100.0	247	7	ADI30575	Adi30575 Human sta
14	1268	100.0	247	7	ABO84399	Abo84399 Human sta
15	1268	100.0	247	8	ADQ21382	Adq21382 Human sof
16	1231	97.1	247	7	ADD48080	Add48080 Rat Prote
17	937	73.9	276	3	AAB56848	Aab56848 Human pro
18	680.5	53.7	261	1	AAP82968	Aap82968 Corpuscle
19	662.5	52.2	256	4	AAB62474	Aab62474 Coho salm
20	628	49.5	170	3	AYY55749	Aay55749 A. austra
21	628	49.5	170	7	ADI30574	Adi30574 Australia
22	358	28.2	70	4	AAM18134	Aam18134 Peptide #
23	358	28.2	70	4	ABB37166	Abb37166 Peptide #
24	358	28.2	70	4	AAM30637	Aam30637 Peptide #
25	358	28.2	70	4	ABB31928	Abb31928 Peptide #
26	358	28.2	70	4	ABB22472	Abb22472 Protein #
27	358	28.2	70	4	AAM70300	Aam70300 Human bon
28	358	28.2	70	4	AAM57878	Aam57878 Human bra
29	358	28.2	70	4	ABG52000	Abg52000 Human liv
30	358	28.2	70	4	AAM05763	Aam05763 Peptide #
31	358	28.2	70	5	ABG39940	Abg39940 Human pep
32	354.5	28.0	296	3	AYY67926	Aay67926 Mouse sta
33	354.5	28.0	296	4	AAB61623	Aab61623 Murine st
34	354	27.9	293	2	AYY41255	Aay41255 Adipogene
35	354	27.9	293	3	AAB26872	Aab26872 Human adi
36	354	27.9	293	4	AAB93965	Aab93965 Human pro
37	354	27.9	302	3	AYY67925	Aay67925 Human sta
38	354	27.9	302	4	AAB98971	Aab98971 Human adi
39	354	27.9	302	4	AAB61621	Aab61621 Human sta
40	354	27.9	302	4	AAB31797	Aab31797 Amino aci
41	354	27.9	302	4	AAB95330	Aab95330 Human pro
42	354	27.9	302	5	ABJ05546	Abj05546 Breast ca
43	354	27.9	302	5	AAE26113	Aae26113 Human BS2
44	354	27.9	302	6	ABR47601	Abr47601 Breast ca
45	354	27.9	302	6	ADA00844	Ada00844 Human bre

#### ALIGNMENTS

RESULT 1

AAR84522

ID AAR84522 standard; protein; 247 AA.

XX

AC AAR84522;

XX

DT 19-APR-1996 (first entry)

XX

DE Stanniocalcin from Corpuscles of Stannius.

XX

KW stanniocalcin; Corpuscles of Stannius; hypocalcaemia; hypercalcaemia;  
KW electrolyte disorder; osteoporosis; Paget's disease; treatment.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Region 1. .33  
FT /label= prepro\_region  
FT Protein 34. .247  
FT /label= mature\_stanniocalcin  
XX  
PN WO9524411-A1.  
XX  
PD 14-SEP-1995.  
XX  
PF 09-MAY-1994; 94WO-US005136.  
XX  
PR 08-MAR-1994; 94US-00208005.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Olsen H, Adams MD;  
XX  
DR WPI; 1995-328227/42.  
DR N-PSDB; AAT02438.  
XX  
PT Human corpuscles of Stannius polypeptide(s) - used to treat  
PT hypercalcaemia, hypocalcaemia and other electrolyte disorders.  
XX  
PS Claim 14; Fig 1; 41pp; English.  
XX  
CC Stanniocalcin, a Corpuscles of Stannius polypeptide is encoded by  
CC AAT02438. Stanniocalcin functions as a hypocalcaemic agent, and can be  
CC used for the treatment of e.g. electrolyte disorders which lead to renal,  
CC bone and heart diseases, hypertension, hypercalcaemia and disorders due  
CC to elevated bone resorption, e.g. osteoporosis and Paget's disease.  
XX  
SQ Sequence 247 AA;  
  
Query Match 100.0%; Score 1268; DB 2; Length 247;  
Best Local Similarity 100.0%; Pred. No. 9.3e-124;  
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRAAQNQSAEVVRCLNSALQVGCGAFACL 60  
| |||||||  
Db 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRAAQNQSAEVVRCLNSALQVGCGAFACL 60  
  
Qy 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120  
| |||||||  
Db 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120  
  
Qy 121 IAEVQEECYSKLNVCIAKRNP EAITEVVQLPNHFSNRYYNRLVRSLL ECDED TVSTIRD 180  
| |||||||  
Db 121 IAEVQEECYSKLNVCIAKRNP EAITEVVQLPNHFSNRYYNRLVRSLL ECDED TVSTIRD 180  
  
Qy 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240  
| |||||||  
Db 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240  
  
Qy 241 RTSHESA 247  
| |||||  
Db 241 RTSHESA 247

RESULT 2  
AAB23264  
ID AAB23264 standard; protein; 247 AA.  
XX  
AC AAB23264;  
XX  
DT 02-FEB-2001 (first entry)  
XX  
DE Human stanniocalcin.  
XX  
KW Human; stanniocalcin; STC; osteogenesis; bone disease; osteoporosis;  
KW mineral metabolism regulator; prophylaxis; therapy.  
XX  
OS Homo sapiens.  
XX  
PN JP2000229880-A.  
XX  
PD 22-AUG-2000.  
XX  
PF 10-FEB-1999; 99JP-00033262.  
XX  
PR 10-FEB-1999; 99JP-00033262.  
XX  
PA (SNOW ) SNOW BRAND MILK PROD CO LTD.  
XX  
DR WPI; 2000-605236/58.  
DR N-PSDB; AAA97594.  
XX  
PT An osteogenesis promotor useful in the prevention and/or treatment of  
PT bone diseases such as osteoporosis.  
XX  
PS Example 1; Page 5-6; 6pp; Japanese.  
XX  
CC The invention relates to a novel osteogenesis-promoting composition which  
CC contains stanniocalcin (STC) as the active component. Stanniocalcin is a  
CC possible regulator of mineral metabolism. The composition is useful as a  
CC prophylactic and/or therapeutic agent for bone diseases such as  
CC osteoporosis. The present sequence represents human stanniocalcin which  
CC was used in an exemplification of the invention  
XX  
SQ Sequence 247 AA;  
  
Query Match 100.0%; Score 1268; DB 3; Length 247;  
Best Local Similarity 100.0%; Pred. No. 9.3e-124;  
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60  
|||  
Db 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60  
  
QY 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120  
|||  
Db 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120  
  
QY 121 IAEVQEECYSKLNVCIAKRNPEAITEVVQLPNHFSRYYNRLVRSLLCEDDETVSTIRD 180  
|||

Db 121 IAEVQEECYSKLNVCIAKRNPEAITEVVQLPNHFSNRYNRLVRSLLCEDDETVSTIRD 180  
Qy 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240  
Db 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240  
Qy 241 RTSHESA 247  
Db 241 RTSHESA 247

RESULT 3

AAY55750

ID AAY55750 standard; protein; 247 AA.

XX

AC AAY55750;

XX

DT 11-FEB-2000 (first entry)

XX

DE Human stanniocalcin polypeptide.

XX

KW Stanniocalcin-alpha polypeptide; teleocalcin; hypocalcin; hypercalcemic;  
KW anti-hypercalcemic glycoprotein hormone; corpuscles of stannius; PTH;  
KW parathyroid hormone; bone reabsorption; osteoporosis; gene therapy; bone;  
KW electrolyte disorder; renal; heart disease; osteopetrosis; human;  
KW Paget's disease; hypercalcemia.

XX

OS Homo sapiens.

XX

PN US5994103-A.

XX

PD 30-NOV-1999.

XX

PF 02-JUN-1995; 95US-00460529.

XX

PR 10-NOV-1994; 94WO-US013206.

XX

PA (HUMA-) HUMAN GENOME SCI INC.

XX

PI Fleischmann RD, Olsen HS;

XX

DR WPI; 2000-038260/03.

XX

PT Isolated nucleic acids encoding human stanniocalcin-alpha useful for  
PT treating electrolyte disorders which lead to renal, bone and heart  
PT diseases, osteoporosis and Paget's disease.

XX

PS Disclosure; Fig 3; 21pp; English.

XX

CC The invention provides a human stanniocalcin-alpha polypeptide (also  
CC called teleocalcin and hypocalcin). Stanniocalcin-alpha is an anti-  
CC hypercalcemic glycoprotein hormone produced by the corpuscles of  
CC stannius. It has a similar reported biological activity to that of  
CC parathyroid hormone (PTH) and both these proteins exhibit dual functions  
CC in mammals. They exert hypercalcemic activity due to stimulation of bone  
CC reabsorption. Further PTH has a biphasic action on bone metabolism (i.e.  
CC at low doses it increases bone formation and at high doses it increases

CC bone reabsorption. Accordingly, human stanniocalcin-alpha and antagonists  
CC of it (under different circumstances) may be used to treat osteoporosis.  
CC The DNA may be used to produce human stanniocalcin-alpha according to  
CC standard recombinant DNA methodologies. The human stanniocalcin-alpha may  
CC be produced either in vitro in a fermentation culture or in vivo as part  
CC of a gene therapy protocol, and may be used to treat electrolyte  
CC disorders which lead to renal, bone and heart diseases. Due to the  
CC biphasic nature of stanniocalcin-alpha it may be used to treat  
CC osteoporosis, osteopetrosis and Paget's disease. Alternatively, the  
CC polypeptides may be used as antigens in the production of antibodies to  
CC stanniocalcin-alpha and to assay for agonists and antagonists of its  
CC activity. The antibodies and antagonists may be used to inhibit the  
CC activity of stanniocalcin-alpha and may be used to treat osteoporosis and  
CC hypercalcemia. The present sequence represents a human stanniocalcin

xx

SQ Sequence 247 AA;

Query Match 100.0%; Score 1268; DB 3; Length 247;  
Best Local Similarity 100.0%; Pred. No. 9.3e-124;  
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRAAQNSAEVVRCLNSALQVGCGFACL 60

Qy 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFRAIRRCSFTQRM 120

Qy 121 IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLCDEDTVSTIRD 180

Qy 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLGEEDSPSHIK 240

Qy 241 RTSHESA 247

22

## RESULT 4

AAV

ID AAY57166

xx

AC . AAY57166;

xx

DT 11-FEB-2000 (first entry)

xx

DE Human corpuscles of stanius polypeptide.  
XX  
KW Corpuscles of stanius polypeptide; calcium; inhibition; human; renal;

KW

XX

OS

PN US5994301-A.  
XX  
PD 30-NOV-1999.  
XX  
PF 28-APR-1995; 95US-00431117.  
XX  
PR 08-MAR-1994; 94US-00208005.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Adams MD, Olsen HS;  
XX  
DR WPI; 2000-038269/03.  
DR N-PSDB; AAZ39520.  
XX  
PT Human corpuscles of stanius polypeptides used to inhibit calcium uptake.  
XX  
PS Claim 4; Fig 1A-B; 23pp; English.  
XX  
CC This represents a human corpuscles of stanius polypeptide, having a  
CC calcium uptake inhibitory activity. The cDNA is deposited under the  
CC accession number ATCC Deposit No. 75652. The polypeptide can be used in a  
CC method for the treatment of a patient having need to inhibit uptake of  
CC calcium. The method is also used for the therapeutic treatment of renal,  
CC bone, and heart diseases, and the antagonist (may be an antibody) may be  
CC used for treating hypocalcemia., and osteoperosis  
XX  
SQ Sequence 247 AA;

Query Match 100.0%; Score 1268; DB 3; Length 247;  
Best Local Similarity 100.0%; Pred. No. 9.3e-124;  
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCALQVGCGAFACL 60  
Db 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCALQVGCGAFACL 60  
Qy 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120  
Db 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120  
Qy 121 IAEVQEECYSKLNVCIAKRNPAAITEEVVQLPNHFSNRYYNRLVRSLLCDEDTVSTIRD 180  
Db 121 IAEVQEECYSKLNVCIAKRNPAAITEEVVQLPNHFSNRYYNRLVRSLLCDEDTVSTIRD 180  
Qy 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240  
Db 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240  
Qy 241 RTSHESA 247  
Db 241 RTSHESA 247

RESULT 5  
AAY92901  
ID AAY92901 standard; protein; 247 AA.

XX  
AC AAY92901;  
XX  
DT 26-SEP-2000 (first entry)  
XX  
DE Human stanniocalcin protein.  
XX  
KW PCR primer; human; stanniocalcin; inhibitor; differentiation; maturation;  
KW adipocyte; obesity; diabetes; hypertension; heart disease.  
XX  
OS Homo sapiens.  
XX  
PN WO200016795-A1.  
XX  
PD 30-MAR-2000.  
XX  
PF 17-SEP-1999; 99WO-JP005080.  
XX  
PR 17-SEP-1998; 98JP-00263004.  
XX  
PA (SNOW ) SNOW BRAND MILK PROD CO LTD.  
XX  
PI Goto M, Tomoyasu A, Yamaguchi K, Kinosaki M, Nakagawa N;  
XX  
DR WPI; 2000-283445/24.  
DR N-PSDB; AAA11145.  
XX  
PT Treating or preventing obesity, which is a risk factor for diabetes,  
PT hypertension and heart disease, comprises administering an agent  
PT containing stanniocalcin.  
XX  
PS Example 1; Page 16; 19pp; Japanese.  
XX  
CC This sequence represents the human stanniocalcin protein. Stanniocalcin  
CC is an inhibitor of the differentiation and maturation of adipocytes. The  
CC protein is used for preventing and treating obesity which is a risk  
CC factor for diabetes, hypertension, and heart disease. The coding sequence  
CC was isolated from IMR-90 cells  
XX  
SQ Sequence 247 AA;  
  
Query Match 100.0%; Score 1268; DB 3; Length 247;  
Best Local Similarity 100.0%; Pred. No. 9.3e-124;  
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCALQVGCGAFACL 60  
| |||||||  
Db 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCALQVGCGAFACL 60  
  
Qy 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120  
| |||||||  
Db 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120  
  
Qy 121 IAEVQEECYSKLNVCIAKRNP EAITEVVQLPNHFSNRYYNRLVRSLL ECDEDTVSTIRD 180  
| |||||||  
Db 121 IAEVQEECYSKLNVCIAKRNP EAITEVVQLPNHFSNRYYNRLVRSLL ECDEDTVSTIRD 180



CC encephalomyelitis, spinal cord diseases, mental retardation such as  
CC Down's syndrome, Tay-Sachs disease, neuromuscular diseases such as  
CC muscular dystrophy, myasthenia gravis, deficiencies or disorders of  
CC immune system such as Addison's disease, hemolytic anemia, rheumatoid  
CC arthritis, dermatitis, glomerulonephritis, Goodpasture's Syndrome,  
CC Grave's disease, multiple sclerosis, autoimmune thyroiditis, systemic  
CC lupus erythematosus, insulin dependent diabetes mellitus, allergic  
CC reactions and conditions such as asthma, for treating and/or preventing  
CC organ rejection or graft-versus-host disease, hyperproliferative diseases  
CC such as purpura, Gaucher's disease, cardiovascular disorders such as  
CC arrhythmias, telangiectasia, vasculitis, and for treatment of disease or  
CC disorders with neovascularization. The composition can be used to treat  
CC hemangioma, psoriasis, angiofibroma, atherosclerotic plaques, delayed  
CC wound healing, granulations, Osler-Weber syndrome, solid tumors such as  
CC Kaposi's sarcoma, cancer, AIDS, neurodegenerative disorders such as  
CC Alzheimer's disease, Parkinson's disease, wound healing, and for treating  
CC or detecting infectious agents. The present sequence represents the human  
CC STC polypeptide

xx

SQ Sequence 247 AA;

```
Query Match          100.0%;  Score 1268;  DB 4;  Length 247;
Best Local Similarity 100.0%;  Pred. No. 9.3e-124;
Matches 247;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;
```

Qy 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRSVAAQNSAEVVRCLNSALQVGCGFACL 60  
|||||

Db 1 MLQNSAVLLVLI SASTHEAEQNDSVSPRKSRAAQNSAEVVRCLNSALQVGCGAFL 60

Db 61 ENSTCDTDGYDICKSFLYSAAKFDTQGKAFVKESSLKCIANGVTSKVFLAIRRCSTFQRM 120

DB 121 IAEVQEECYSKLNVCSTAKRNPEATTEVVQLPNHFNSRKYYNRLVRSLLECDEDIVSTIRD 180

QY 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADENRRRTNEPQKLKVLLRNLGEEDSFHIK 240  
Pb 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADENRRRTNEPQKLKVLLRNLGEEDSFHIK 240

181 SEMERKIGPNEASLPHIQLPDRCAQTHPRADFNRRKRNQFQRKERVLEERNGEEDSFHTR 240

241 RISHESA 247

Ph 241 BTSHES

## RESULT 7

AAB62690

ID AAB62690 standard; protein; 247 AA.

xx

AC AAB62690;

xx

DT 06-AUG-2001 (first entry)

xx

DE Lng108, a diagnostic marker for cancer.

xx

KW Lng108; cancer; diagnostic marker; cytotoxic; immune response; imaging.

XX  
OS Homo sapiens.  
XX  
PN WO200132209-A1.  
XX  
PD 10-MAY-2001.  
XX  
PF 03-NOV-2000; 2000WO-US030482.  
XX  
PR 04-NOV-1999; 99US-0163444P.  
XX  
PA (DIAD-) DIADEXUS INC.  
XX  
PI Recipon H, Macina RA, Chen S, Sun Y;  
XX  
DR WPI; 2001-316386/33.  
DR N-PSDB; AAF83823.  
XX  
PT Novel assay for diagnosing and monitoring cancer, involves determining  
PT levels of Lng108 in cells, tissues or bodily fluids of the patient, and  
PT comparing with control.  
XX  
PS Disclosure; Page 33-34; 36pp; English.  
XX  
CC The invention relates to diagnosing the presence of cancer or diagnosing  
CC metastases of cancer in a patient that involves determining levels of  
CC Lng108 in a sample of cells, tissues or bodily fluids in a patient, and  
CC comparing the determined levels with levels of Lng108 a normal human  
CC control. The method is useful for diagnosing the presence of cancer,  
CC diagnosing metastases of cancer, staging cancer, monitoring cancer, and  
CC monitoring a change in stage of the cancer, in a patient. A therapeutic  
CC agent which is an antibody labeled with paramagnetic ions or a  
CC radioisotope, and conjugated with a cytotoxic agent is useful for imaging  
CC cancer in a patient. A molecule which downregulates the expression or  
CC activity of Lng108, is useful for treating cancer in a patient. Lng108  
CC protein is useful for inducing an immune response against a target cell  
CC expressing Lng108. The present sequence represents the human Lng108  
CC polypeptide  
XX  
SQ Sequence 247 AA;

Query Match 100.0%; Score 1268; DB 4; Length 247;  
Best Local Similarity 100.0%; Pred. No. 9.3e-124;  
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRAAQNSAEVVRCALQVGCGAFACL 60  
|||  
Db 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRAAQNSAEVVRCALQVGCGAFACL 60  
  
Qy 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120  
|||  
Db 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120  
  
Qy 121 IAEVQEECYSKLNVCIAKRNPPEAITEVVQLPNHFSNRYYNRLVRSLLCEDEDTVSTIRD 180  
|||  
Db 121 IAEVQEECYSKLNVCIAKRNPPEAITEVVQLPNHFSNRYYNRLVRSLLCEDEDTVSTIRD 180



Query Match 100.0%; Score 1268; DB 5; Length 247;  
 Best Local Similarity 100.0%; Pred. No. 9.3e-124;  
 Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL	60
Db	1	MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL	60
Qy	61	ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM	120
Db	61	ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM	120
Qy	121	IAEVQEECYSKLNVCIAKRNP EAITEVVQLPNHFSNRYYNRLVRSLL ECDEDTVSTIRD	180
Db	121	IAEVQEECYSKLNVCIAKRNP EAITEVVQLPNHFSNRYYNRLVRSLL ECDEDTVSTIRD	180
Qy	181	SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK	240
Db	181	SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK	240
Qy	241	RTSHESA 247	
Db	241	RTSHESA 247	

RESULT 9  
 ABP97748  
 ID ABP97748 standard; protein; 247 AA.  
 XX  
 AC ABP97748;  
 XX  
 DT 28-MAY-2003 (first entry)  
 XX  
 DE Amino acid sequence of human STC1 polypeptide.  
 XX  
 KW Human; angiogenesis; wound healing; retinopathy; ischemia; inflammation;  
 KW microvasculopathy; bone healing; skin inflammation; HOG3; HOG8; HOG18;  
 KW follicular development; CA9; HXB; IGFBP5; HFARP; STC1; mig-6; SSR4;  
 KW cancer.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003010205-A1.  
 XX  
 PD 06-FEB-2003.  
 XX  
 PF 26-JUL-2002; 2002WO-US023786.  
 XX  
 PR 26-JUL-2001; 2001US-0307600P.  
 PR 24-JUL-2002; 2002US-00201642.  
 XX  
 PA (UYDU-) UNIV DUKE MEDICAL CENT.  
 XX  
 PI Riggins GJ, Lal A;  
 XX  
 DR WPI; 2003-239423/23.

DR N-PSDB; ABZ77288.

XX

PT Inhibiting angiogenesis for treating wound healing, retinopathy, ischemia, inflammation, microvasculopathy, bone healing, skin inflammation or follicular development by providing to a subject an antisense polynucleotide.

XX

PS Claim 4; Page 61; 66pp; English.

XX

CC The present sequence is a human STC1 polypeptide. It is used in the method of the invention. The specification describes a method modulating angiogenesis associated with wound healing, retinopathy, ischemia, inflammation, microvasculopathy, bone healing, skin inflammation or follicular development. The method comprises providing to a subject HOG3, HOG8, HOG18, CA9, HXB, IGFBP5, HFARP, STC1, mig-6 or SSR4. The methods, antisense polynucleotides, polypeptides and antibodies are useful for treating wound healing, retinopathy, ischemia, inflammation, microvasculopathy, bone healing, skin inflammation or follicular development, or cancer such as breast, colon or lung cancer, or glioblastoma

XX

SQ Sequence 247 AA;

Query Match 100.0%; Score 1268; DB 6; Length 247;  
Best Local Similarity 100.0%; Pred. No. 9.3e-124;  
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRAAQNSAEVVRCILNSALQVGCGAFACL 60  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRAAQNSAEVVRCILNSALQVGCGAFACL 60

Qy .61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120

Qy 121 IAEVQEECYSKLNVCISIARKNPEAITEVVQLPNHFSNRYYNRLVRSLLCEDDEDTVSTIRD 180  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 121 IAEVQEECYSKLNVCISIARKNPEAITEVVQLPNHFSNRYYNRLVRSLLCEDDEDTVSTIRD 180

Qy 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240

Qy 241 RTSHESA 247  
||| |||

Db 241 RTSHESA 247

RESULT 10

ABR47600

ID ABR47600 standard; protein; 247 AA.

XX

AC ABR47600;

XX

DT 12-JUN-2003 (first entry)

XX

DE Breast cancer associated protein sequence SEQ ID NO:441.

XX Human; breast cancer; cytostatic; gene therapy.  
XX  
OS Homo sapiens.  
XX  
PN WO2003004989-A2.  
XX  
PD 16-JAN-2003.  
XX  
PF 21-JUN-2002; 2002WO-US019669.  
XX  
PR 21-JUN-2001; 2001US-0299887P.  
PR 27-JUN-2001; 2001US-0301572P.  
PR 18-JUL-2001; 2001US-0306501P.  
PR 25-SEP-2001; 2001US-0325002P.  
PR 05-MAR-2002; 2002US-0362585P.  
PR 14-MAY-2002; 2002US-0380391P.  
XX  
PA (MILL-) MILLENIUM PHARM INC.  
XX  
PI Lillie J, Gannavarapu M, Glatt K, Hoersh S, Kamatkar S;  
PI Mertens M, Monahan JE, Myer V, Wang Y, Xu Y, Zhao X, Meyers RE;  
PI Bast RC, Hortobagyi GN, Pusztai L, Meric F, Sahin A, Mills GB;  
XX  
DR WPI; 2003-210381/20.  
DR N-PSDB; ACC50301.  
XX  
PT Breast cancer diagnosis or treatment by comparing the level of expression  
PT of a marker in a patient sample with that in the control non-breast  
PT cancer sample.  
XX  
PS Claim 1; SEQ ID NO 441; 128pp; English.  
XX  
CC The present invention describes a method for assessing whether a patient  
CC is afflicted with breast cancer. The method comprises comparing the level  
CC of expression of a marker (gene/polypeptide see ACC50076 to ACC50334 and  
CC ABR47386 to ABR47632) in a patient sample and the normal level of  
CC expression of the marker in a control non-breast cancer sample, where a  
CC significant increase in the level of expression of the marker in the  
CC patient sample and the normal level is an indication that the patient is  
CC afflicted with breast cancer. The breast cancer associated sequences from  
CC the present invention have cytostatic activities and can be used in gene  
CC therapy. The method is useful for diagnosing and treating breast cancer.  
CC N.B. The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at [ftp://wipo.int/pub/published\\_pct\\_sequences](ftp://wipo.int/pub/published_pct_sequences)  
XX  
SQ Sequence 247 AA;

Query Match 100.0%; Score 1268; DB 6; Length 247;  
Best Local Similarity 100.0%; Pred. No. 9.3e-124;  
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL	60
Db	1	MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL	60



PT disease, hypercalcemia and sarcoidosis.

XX

PS Claim 13; Fig 1; 26pp; English.

XX

CC The present invention relates to the isolation of human Corpuscles of  
CC Stannius protein, and the polynucleotide sequence encoding it. Human  
CC Corpuscles of Stannius protein inhibits calcium uptake and reduces renal  
CC excretion of phosphate. The polynucleotide sequence is useful for  
CC encoding Corpuscles of Stannius protein for therapeutic purposes, e.g. in  
CC the treatment of electrolyte disorders that lead to renal, bone or heart  
CC disease, such as arterial hypertension, disorders due to elevated bone  
CC resorption (e.g. osteoporosis and Paget's disease), and hypercalcaemia  
CC (e.g. hyperparathyroidism, hypervitaminosis D), tumours that raise serum  
CC calcium levels by destroying bone, sarcoidosis, hyperthyroidism, adrenal  
CC insufficiency, loss of serum albumin secondary to renal diseases, or  
CC excessive GI calcium absorption and elevated concentration of plasma  
CC proteins. The encoded polypeptide exhibits a high degree of homology to  
CC Stanniocalcin from *Anguilla australis* and from *Oncorhynchus kisutch*. The  
CC present sequence represents human corpuscles of stannius protein

XX

SQ Sequence 247 AA;

Query Match 100.0%; Score 1268; DB 6; Length 247;  
Best Local Similarity 100.0%; Pred. No. 9.3e-124;  
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCILNSALQVGCGAFACL 60  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCILNSALQVGCGAFACL 60

Qy 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120

Qy 121 IAEVQEECYSKLNVCIAKRNPPEAITEVVQLPNHFSNRYYNRLVRSLLCEDDEDTVSTIRD 180  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 121 IAEVQEECYSKLNVCIAKRNPPEAITEVVQLPNHFSNRYYNRLVRSLLCEDDEDTVSTIRD 180

Qy 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240

Qy 241 RTSHESA 247

||| |||

Db 241 RTSHESA 247

RESULT 12

ADD48082

ID ADD48082 standard; protein; 247 AA.

XX

AC ADD48082;

XX

DT 29-JAN-2004 (first entry)

XX

DE Human Protein P52823, SEQ ID NO 13779.

XX

KW Human; pain; neuronal tissue; gene therapy;  
KW spinal segmental nerve injury; chronic constriction injury; CCI;  
KW spared nerve injury; SNI; Chung.  
XX  
OS Homo sapiens.  
XX  
PN WO2003016475-A2.  
XX  
PD 27-FEB-2003.  
XX  
PF 14-AUG-2002; 2002WO-US025765.  
XX  
PR 14-AUG-2001; 2001US-0312147P.  
PR 01-NOV-2001; 2001US-0346382P.  
PR 26-NOV-2001; 2001US-0333347P.  
XX  
PA (GEHO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
XX  
PI Woolf C, D'urso D, Befort K, Costigan M;  
XX  
DR WPI; 2003-268312/26.  
DR GENBANK; P52823.  
XX  
PT New composition comprising two or more isolated polypeptides, useful for  
PT preparing a medicament for treating pain in an animal.  
XX  
PS Claim 1; Page; 1017pp; English.  
XX  
CC The invention discloses a composition comprising two or more isolated rat  
CC or human polynucleotides or a polynucleotide which represents a fragment,  
CC derivative or allelic variation of the nucleic acid sequence. Also  
CC claimed are a vector comprising the novel polynucleotide, a host cell  
CC comprising the vector, a method for identifying a nucleotide sequence  
CC which is differentially regulated in an animal subjected to pain and a  
CC kit to perform the method, an array, a method for identifying an agent  
CC that increases or decreases the expression of the polynucleotide sequence  
CC that is differentially expressed in neuronal tissue of a first animal  
CC subjected to pain, a method for identifying a compound which regulates  
CC the expression of a polynucleotide sequence which is differentially  
CC expressed in an animal subjected to pain, a method for identifying a  
CC compound that regulates the activity of one or more of the  
CC polynucleotides, a method for producing a pharmaceutical composition, a  
CC method for identifying a compound or small molecule that regulates the  
CC activity in an animal of one or more of the polypeptides given in the  
CC specification, a method for identifying a compound useful in treating  
CC pain and a pharmaceutical composition comprising the one or more  
CC polypeptides or their antibodies. The polynucleotide or the compound that  
CC modulates its activity is useful for preparing a medicament for treating  
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction  
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
CC therapy). The sequence presented is a human protein (shown in Table 2 of  
CC the specification) which is differentially expressed during pain. Note:  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic form directly from WIPO at  
CC [ftp://wipo.int/pub/published\\_pct\\_sequences](ftp://wipo.int/pub/published_pct_sequences).  
XX

SQ Sequence 247 AA;

Query Match 100.0%; Score 1268; DB 7; Length 247;  
Best Local Similarity 100.0%; Pred. No. 9.3e-124;  
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60

Qy 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120

Qy 121 IAEVQEECYSKLNVCIAKRNP EAITEVVQLPNHFSNRYYNRLVRSLL ECDEDTVSTIRD 180  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 121 IAEVQEECYSKLNVCIAKRNP EAITEVVQLPNHFSNRYYNRLVRSLL ECDEDTVSTIRD 180

Qy 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240

Qy 241 RTSHESA 247  
||| |||  
Db 241 RTSHESA 247

RESULT 13

ADI30575

ID ADI30575 standard; protein; 247 AA.

XX

AC ADI30575;

XX

DT 22-APR-2004 (first entry)

XX

DE Human stannicoalcin protein.

XX

KW human; stanniocalcin-alpha; electrolyte imbalance; hypertension;  
KW hyperglycaemia; migraine; renal disease; heart disease; bone disease;  
KW osteoporosis; hypoglycaemia; Paget's disease.

XX

OS Homo sapiens.

XX

PN US2003181663-A1.

XX

PD 25-SEP-2003.

XX

PF 18-APR-2003; 2003US-00418226.

XX

PR 10-NOV-1994; 94WO-US013206.

PR 02-JUN-1995; 95US-00460529.

PR 28-JUL-1999; 99US-00361736.

XX

PA (HUMA-) HUMAN GENOME SCI INC.

XX

PI Olsen HS, Fleischmann RD;

XX

DR WPI; 2003-852260/79.

XX

PT New human stanniocalcin-alpha polypeptide, useful in regulating  
PT electrolyte imbalances, or for diagnosing and treating a disease  
PT associated with mutated forms of stanniocalcin-alpha sequences, e.g.  
PT renal disease or osteoporosis.

XX

PS Disclosure; SEQ ID NO 10; 22pp; English.

XX

CC The invention comprises the amino acid and coding sequence of a human  
CC stanniocalcin-alpha protein. The DNA and protein sequences of the  
CC invention are useful for regulating electrolyte imbalances to treat  
CC hypertension, hyperglycaemia or migraine. The DNA and protein sequences  
CC are also useful in diagnosing and treating a disease associated with  
CC mutated forms of stanniocalcin-alpha sequences, such as: renal disease,  
CC heart disease or bone disease (e.g. osteoporosis). The DNA and protein  
CC sequences may also be used to treat hypoglycaemia or Paget's disease. The  
CC present amino acid sequence represents a human stanniocalcin protein.

XX

SQ Sequence 247 AA;

Query Match 100.0%; Score 1268; DB 7; Length 247;  
Best Local Similarity 100.0%; Pred. No. 9.3e-124;  
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCALQVGCGAFACL 60  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCALQVGCGAFACL 60

Qy 61 ENSTCDTDMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 61 ENSTCDTDMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120

Qy 121 IAEVQEECYSKLNVCIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLCEDDEDVSTIRD 180  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 121 IAEVQEECYSKLNVCIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLCEDDEDVSTIRD 180

Qy 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240

Qy 241 RTSHESA 247

||| |||

Db 241 RTSHESA 247

RESULT 14

ABO84399

ID ABO84399 standard; protein; 247 AA.

XX

AC ABO84399;

XX

DT 29-JUL-2004 (first entry)

XX

DE Human stanniocalcin protein.

XX

KW Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;

KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;  
KW surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;  
KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;  
KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;  
KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;  
KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;  
KW pulmonary transplantation rejection.  
XX  
OS Homo sapiens.  
XX  
PN WO200285309-A2.  
XX  
PD 31-OCT-2002.  
XX  
PF 23-APR-2002; 2002WO-US013143.  
XX  
PR 24-APR-2001; 2001US-0286036P.  
XX  
PA (EPIG-) EPIGENESIS PHARM INC.  
XX  
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
PI Miller S, Tang L, Shahabuddin S;  
XX  
DR WPI; 2003-093058/08.  
DR N-PSDB; ABD20997.  
XX  
PT Pharmaceutical composition for treating asthma, has antisense  
PT oligonucleotide containing less percentage of adenosine, targeted to  
PT nucleic acids associated with lung airway or lung dysfunction, and  
PT bronchodilating agent.  
XX  
PS Claim 15; SEQ ID NO 6; 763pp; English.  
XX  
CC This invention describes a novel composition (a) a first active agent,  
CC comprising oligonucleotides, effective for alleviating  
CC bronchoconstriction, respiratory tract inflammation, allergies and  
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,  
CC surfactant depletion or hyposecretion, when administered to a mammal. The  
CC oligonucleotides are derived from a gene encoding or regulating  
CC expression of a target polypeptide associated with lung airway or lung  
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.  
CC The invention also describes a kit, that comprises: (a) a delivery  
CC device, in separate containers, (b) the oligonucleotides, (c)  
CC instructions for adding a carrier and for use of the kit. The composition  
CC of the invention has antiallergic, antiinflammatory, antiasthmatic,  
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a  
CC beta-adrenergic agonist. The composition is useful for preventing or  
CC treating a respiratory, lung or malignant disease. The administered  
CC composition comprises oligo and is administered to reduce the production  
CC or availability, or to increase the degradation of the target mRNA or to  
CC reduce the amount of target polypeptide present in the lungs. The  
CC pulmonary obstruction, and/or bronchoconstriction and/or lung  
CC inflammation, allergies and/or surfactant hypoproduction are associated  
CC with a disease or condition such as pulmonary vasoconstriction,  
CC inflammation, allergies, asthma, impeded respiration, respiratory  
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary  
CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary



XX  
PI Aziz N, Ginsburg WM, Zlotnik A;  
XX  
DR WPI; 2004-441208/41.  
XX  
PT Early detection of soft tissue sarcoma comprises determining expression  
PT of a gene in a first soft tissue sample and a normal soft tissue sample  
PT and comparing the gene expression, also useful in treating soft tissue  
PT sarcoma.  
XX  
PS Example 2; SEQ ID NO 4202; 210pp; English.  
XX  
CC The invention relates to a novel method for detecting soft tissue sarcoma  
CC which comprises obtaining a first soft tissue sample from an individual  
CC and a normal soft tissue sample from the same or different individual,  
CC determining the expression of a gene in both samples and comparing the  
CC expression of the gene in both soft tissue samples, where a higher level  
CC of protein expression in the first soft tissue sample indicates the  
CC presence of soft tissue sarcoma. The method of the invention has  
CC cytostatic applications and may be useful for detecting soft tissue  
CC sarcoma, possibly via gene therapy or vaccine production. The nucleic  
CC acid sequences may be useful in diagnostic and screening applications.  
CC The current sequence is that of a human soft tissue sarcoma-upregulated  
CC protein of the invention. The current sequence is not shown within the  
CC specification per se but was submitted in CD format by the inventor.  
XX  
SQ Sequence 247 AA;  
  
Query Match 100.0%; Score 1268; DB 8; Length 247;  
Best Local Similarity 100.0%; Pred. No. 9.3e-124;  
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRAAQNSAEVVRCLNSALQVGCGAFACL 60  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRAAQNSAEVVRCLNSALQVGCGAFACL 60  
  
Qy 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120  
  
Qy 121 IAEVQEECYSKLNVCIAKRNP EAITEVVQLPNHFSNRYYNRLVRSLL ECDED TVSTIRD 180  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 121 IAEVQEECYSKLNVCIAKRNP EAITEVVQLPNHFSNRYYNRLVRSLL ECDED TVSTIRD 180  
  
Qy 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240  
  
Qy 241 RTSHESA 247  
||| ||| |||  
Db 241 RTSHESA 247

Search completed: January 14, 2005, 22:14:51  
Job time : 235 secs

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OM protein - protein search, using sw model

Run on: January 14, 2005, 22:10:59 ; Search time 40 Seconds  
(without alignments)  
409.514 Million cell updates/sec

Title: US-10-614-990-2

Perfect score: 1268

Sequence: 1 MLQNSAVLLVLVISASATHE.....NLRGEEDSPSHIKRTSHESA 247

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_AA:\*

1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:\*

2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*

3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*

4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*

5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*

6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

8

Result No.	Score	Query			Description	
		Match	Length	DB	ID	
1	1268	100.0	247	2	US-08-208-005C-2	Sequence 2, Appli
2	1268	100.0	247	2	US-09-038-597A-2	Sequence 2, Appli
3	1268	100.0	247	2	US-08-460-529B-10	Sequence 10, Appli
4	1268	100.0	247	2	US-08-431-117A-2	Sequence 2, Appli
5	1268	100.0	247	4	US-09-361-736B-10	Sequence 10, Appli
6	660.5	52.1	204	2	US-08-208-005C-5	Sequence 5, Appli
7	660.5	52.1	204	2	US-09-038-597A-5	Sequence 5, Appli
8	628	49.5	170	2	US-08-460-529B-9	Sequence 9, Appli
9	628	49.5	170	4	US-09-361-736B-9	Sequence 9, Appli
10	354.5	28.0	296	3	US-08-831-132-14	Sequence 14, Appli

11	354.5	28.0	296	3	US-09-416-150-14	Sequence 14, Appl
12	354	27.9	302	3	US-08-831-132-2	Sequence 2, Appli
13	354	27.9	302	3	US-09-416-150-2	Sequence 2, Appli
14	354	27.9	302	4	US-09-193-881-23	Sequence 23, Appl
15	354	27.9	302	4	US-09-361-736B-12	Sequence 12, Appl
16	351.5	27.7	251	4	US-09-361-736B-2	Sequence 2, Appli
17	333.5	26.3	251	2	US-08-460-529B-2	Sequence 2, Appli
18	91	7.2	901	4	US-09-828-062-8	Sequence 8, Appli
19	89.5	7.1	10182	3	US-09-134-001C-3159	Sequence 3159, Ap
20	86	6.8	500	4	US-09-198-452A-299	Sequence 299, App
21	85.5	6.7	311	4	US-09-710-279-2460	Sequence 2460, Ap
22	85.5	6.7	656	3	US-09-134-001C-4322	Sequence 4322, Ap
23	83.5	6.6	290	4	US-09-655-908-6	Sequence 6, Appli
24	83.5	6.6	290	4	US-09-655-908-8	Sequence 8, Appli
25	83.5	6.6	1027	4	US-09-762-724-8	Sequence 8, Appli
26	83.5	6.6	1029	4	US-09-762-724-6	Sequence 6, Appli
27	83	6.5	319	4	US-09-710-279-792	Sequence 792, App
28	83	6.5	319	4	US-09-710-279-2008	Sequence 2008, Ap
29	83	6.5	398	4	US-09-710-279-44	Sequence 44, Appl
30	83	6.5	398	4	US-09-710-279-1498	Sequence 1498, Ap
31	83	6.5	417	3	US-09-134-001C-3810	Sequence 3810, Ap
32	82	6.5	362	3	US-09-134-001C-4670	Sequence 4670, Ap
33	81	6.4	680	3	US-09-298-924-4	Sequence 4, Appli
34	81	6.4	720	2	US-08-840-236-1	Sequence 1, Appli
35	81	6.4	720	2	US-08-505-448A-1	Sequence 1, Appli
36	79.5	6.3	609	4	US-09-538-092-711	Sequence 711, App
37	79.5	6.3	708	1	US-08-145-681-4	Sequence 4, Appli
38	79.5	6.3	708	1	US-08-453-703-4	Sequence 4, Appli
39	79.5	6.3	708	2	US-08-456-106-4	Sequence 4, Appli
40	79.5	6.3	708	3	US-08-456-108-4	Sequence 4, Appli
41	79.5	6.3	708	3	US-09-265-577-4	Sequence 4, Appli
42	79.5	6.3	708	4	US-09-633-739-4	Sequence 4, Appli
43	79	6.2	264	4	US-09-134-000C-5831	Sequence 5831, Ap
44	78.5	6.2	1288	4	US-09-546-934-4	Sequence 4, Appli
45	78	6.2	315	3	US-09-184-964-4	Sequence 4, Appli

#### ALIGNMENTS

#### RESULT 1

US-08-208-005C-2

; Sequence 2, Application US/08208005C

; Patent No. 5837498

; GENERAL INFORMATION:

; APPLICANT: OLSEN, ET. AL.

; TITLE OF INVENTION: Corpuscles of Stannius Protein, Stanniocalcin

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,

; ADDRESSEE: CECCHI, STEWART & OLSTEIN

; STREET: 6 BECKER FARM ROAD

; CITY: ROSELAND

; STATE: NEW JERSEY

; COUNTRY: USA

; ZIP: 07068

; COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 INCH DISKETTE  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WORD PERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/208,005C  
FILING DATE: 8 MARCH 1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: FERRARO, GREGORY D.  
REGISTRATION NUMBER: 36,134  
REFERENCE/DOCKET NUMBER: 325800-78  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-994-1700  
TELEFAX: 201-994-1744  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 247 AMINO ACIDS  
TYPE: AMINO ACID  
STRANDEDNESS:  
TOPOLOGY: LINEAR  
MOLECULE TYPE: PROTEIN  
US-08-208-005C-2

## RESULT 2

US-09-038-597A-2  
; Sequence 2, Application US/09038597A  
; Patent No. 5877290  
; GENERAL INFORMATION:

APPLICANT: OLSEN, ET AL.  
TITLE OF INVENTION: Corpuscles of Stannius Protein,  
TITLE OF INVENTION: Stanniocalcin  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,  
ADDRESSEE: CECCHI, STEWART & OLSTEIN  
STREET: 6 BECKER FARM ROAD  
CITY: ROSELAND  
STATE: NEW JERSEY  
COUNTRY: USA  
ZIP: 07068  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 INCH DISKETTE  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WORD PERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/038,597A  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/208,005  
FILING DATE: 8-MARCH-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: FERRARO, GREGORY D.  
REGISTRATION NUMBER: 36,134  
REFERENCE/DOCKET NUMBER: 325800-78  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-994-1700  
TELEFAX: 201-994-1744  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 247 AMINO ACIDS  
TYPE: AMINO ACID  
STRANDEDNESS:  
TOPOLOGY: LINEAR  
MOLECULE TYPE: PROTEIN  
US-09-038-597A-2



Db ||||||| 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRAAQN SAEVVRCLNSALQVGCGAFACL 60  
Qy 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120  
Db 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120  
Qy 121 IAEVQEECYSKLNVCISI AKRNPEAITEVVQLPNHFSNRYYNRLVRSLL ECDEDTVSTIRD 180  
Db 121 IAEVQEECYSKLNVCISI AKRNPEAITEVVQLPNHFSNRYYNRLVRSLL ECDEDTVSTIRD 180  
Qy 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240  
Db 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240  
Qy 241 RTSHESA 247  
Db 241 RTSHESA 247

RESULT 4

US-08-431-117A-2

; Sequence 2, Application US/08431117A

; Patent No. 5994301

; GENERAL INFORMATION:

; APPLICANT: OLSEN, ET AL.

; TITLE OF INVENTION: Corpuscles of Stannius Protein, Stanniocalcin

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,

; ADDRESSEE: CECCHI, STEWART & OLSTEIN

; STREET: 6 BECKER FARM ROAD

; CITY: ROSELAND

; STATE: NEW JERSEY

; COUNTRY: USA

; ZIP: 07068

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 INCH DISKETTE

; COMPUTER: IBM PS/2

; OPERATING SYSTEM: MS-DOS

; SOFTWARE: WORD PERFECT 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/431,117A

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/208,005

; FILING DATE: 8 MARCH 1994

; ATTORNEY/AGENT INFORMATION:

; NAME: FERRARO, GREGORY D.

; REGISTRATION NUMBER: 36,134

; REFERENCE/DOCKET NUMBER: 325800-296

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 201-994-1700

; TELEFAX: 201-994-1744

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 247 AMINO ACIDS  
; TYPE: AMINO ACID  
; STRANDEDNESS:  
; TOPOLOGY: LINEAR  
; MOLECULE TYPE: PROTEIN  
US-08-431-117A-2

Query Match 100.0%; Score 1268; DB 2; Length 247;  
Best Local Similarity 100.0%; Pred. No. 1.6e-136;  
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60  
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Db 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60  
  
Qy 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120  
||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Db 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120  
  
Qy 121 IAEVQEECYSKLNVCISIARKNPEAITEVVQLPNHFSNRYYNRLVRSLLCEDDEDTVSTIRD 180  
||||||||||||||||||||||||||||||||||||||||||||||||||||  
Db 121 IAEVQEECYSKLNVCISIARKNPEAITEVVQLPNHFSNRYYNRLVRSLLCEDDEDTVSTIRD 180  
  
Qy 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLGEEDSPSHIK 240  
||||||||||||||||||||||||||||||||||||||||||||||||  
Db 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLGEEDSPSHIK 240  
  
Qy 241 RTSHESA 247  
|||||||  
Db 241 RTSHESA 247

## RESULT 5

US-09-361-736B-10

; Sequence 10, Application US/09361736B  
; Patent No. 6613877  
; GENERAL INFORMATION:  
; APPLICANT: Human Genome Sciences, Inc.  
; TITLE OF INVENTION: Human Stanniocalcin-Alpha  
; FILE REFERENCE: PF143P1D1  
; CURRENT APPLICATION NUMBER: US/09/361,736B  
; CURRENT FILING DATE: 1999-07-28  
; PRIOR APPLICATION NUMBER: 08/460,529  
; PRIOR FILING DATE: 1995-06-02  
; PRIOR APPLICATION NUMBER: PCT/ US94/13206  
; PRIOR FILING DATE: 1994-11-30  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 10  
; LENGTH: 247  
; TYPE: PRT  
; ORGANISM: human  
US-09-361-736B-10

Query Match 100.0%; Score 1268; DB 4; Length 247;  
Best Local Similarity 100.0%; Pred. No. 1.6e-136;  
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60  
|  
Db 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60  
  
QY 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120  
|  
Db 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120  
  
QY 121 IAEVQEECYSKLNVCASIARKNPEAITEVVQLPNHFSNRYYNRLVRSLLCEDEDTVSTIRD 180  
|  
Db 121 IAEVQEECYSKLNVCASIARKNPEAITEVVQLPNHFSNRYYNRLVRSLLCEDEDTVSTIRD 180  
  
QY 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240  
|  
Db 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240  
  
QY 241 RTSHESA 247  
|  
Db 241 RTSHESA 247

RESULT 6

US-08-208-005C-5

; Sequence 5, Application US/08208005C

; Patent No. 5837498

; GENERAL INFORMATION:

; APPLICANT: OLSEN, ET AL.

; TITLE OF INVENTION: Corpuscles of Stannius Protein, Stanniocalcin

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,

; ADDRESSEE: CECCHI, STEWART & OLSTEIN

; STREET: 6 BECKER FARM ROAD

; CITY: ROSELAND

; STATE: NEW JERSEY

; COUNTRY: USA

; ZIP: 07068

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 INCH DISKETTE

; COMPUTER: IBM PS/2

; OPERATING SYSTEM: MS-DOS

; SOFTWARE: WORD PERFECT 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/208,005C

; FILING DATE: 8 MARCH 1994

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: FERRARO, GREGORY D.

; REGISTRATION NUMBER: 36,134

; REFERENCE/DOCKET NUMBER: 325800-78

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 201-994-1700

; TELEFAX: 201-994-1744



APPLICATION NUMBER: 08/208,005  
FILING DATE: 8-MARCH-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: FERRARO, GREGORY D.  
REGISTRATION NUMBER: 36,134  
REFERENCE/DOCKET NUMBER: 325800-78  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-994-1700  
TELEFAX: 201-994-1744  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 204 AMINO ACIDS  
TYPE: AMINO ACID  
STRANDEDNESS:  
TOPOLOGY: LINEAR  
MOLECULE TYPE: PROTEIN  
US-09-038-597A-5

Query Match 52.1%; Score 660.5; DB 2; Length 204;  
Best Local Similarity 60.8%; Pred. No. 3.4e-67;  
Matches 118; Conservative 38; Mismatches 37; Indels 1; Gaps 1;

Qy 11 LVISASATHEAEQNDSVSPRSRVAAQNSAEVVRCLNSALQVGCGAFACLENSTCDTDGM 70  
||: :|| : : :: ||||:|| :: : ::|| |||| || |||| |||||||||||||  
Db 12 LVLGTAATFDTDPEEA-SPRRARFSSNSPSDVARCLNGALAVGCGTFACLENSTCDTDGM 70

Qy 71 YDICKSFLYSAAKFDTQGKAFVKESLKCIAANGVTSKVFLAIRRCSTFQRMIAEVQEECYS 130  
:|||: | :||| |:|||| ||||||:||||||||| |||| |||||:|||||||  
Db 71 HDICQLFFHTAATFNTQGKTFVKESLRCIANGVTSKVFTIRRCGVFQRMISEVQEECYS 130

Qy 131 KLNVCIAKRNPAAITEVVQLPNHFSNRYNRLVRSILCDEDTVSTIRDSLMEKIGPNM 190  
:||:| :|: ||||| ||||:| || ||||: |:||| ||||:||: :| | : :||:|  
Db 131 RLDICGVARSNPEAIGEVVQVPAHFPNRYYSTLLQSILLACDEETVAVVRAGLVARLGPDM 190

Qy 191 ASLFHILQTDHCAQ 204  
:|| :|| |||  
Db 191 ETLFQOLLQNKHCPQ 204

#### RESULT 8

US-08-460-529B-9  
; Sequence 9, Application US/08460529B  
; Patent No. 5994103  
; GENERAL INFORMATION:  
; APPLICANT: OLSEN, ET AL.  
; TITLE OF INVENTION: Human Stanniocalcin-alpha  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,  
; ADDRESSEE: CECCHI, STEWART & OLSTEIN  
; STREET: 6 BECKER FARM ROAD  
; CITY: ROSELAND  
; STATE: NEW JERSEY  
; COUNTRY: USA  
; ZIP: 07068  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 INCH DISKETTE

COMPUTER: IBM PS/2  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WORD PERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/460,529B  
FILING DATE: June 2, 1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/13206  
FILING DATE: 10 NOV 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: MULLINS, J.G.  
REGISTRATION NUMBER: 33,073  
REFERENCE/DOCKET NUMBER: 325800-334 (PF143)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-994-1700  
TELEFAX: 201-994-1744  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 170 AMINO ACIDS  
TYPE: AMINO ACID  
STRANDEDNESS:  
TOPOLOGY: LINEAR  
MOLECULE TYPE: PROTEIN  
US-08-460-529B-9

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Query Match          49.5%;  Score 628;  DB 2;  Length 170;
Best Local Similarity  66.5%;  Pred. No. 1.3e-63;
Matches 113;  Conservative 30;  Mismatches 27;  Indels 0;  Gaps 0;

Qy      28 SPRKSRVAAQNSAEVVRCLNSALQVGCGAFACLENSTCDTDGMYDICKSFLYSAAKFDTQ 87
       ||| :| :| : ::| |||| ||||| ||||:|||:|||:|||:|||: ||||| |
Db      1 SPRTARFSASSPSDVARCLNGALQVGCSAFACLDNSTCNDGMHEICRSFLHGAAKFDTQ 60

Qy      88 GKAFVKESLKCIANGVTSKVFIAIRRCSTFQRMIAEVQEECYSKLNVCASIARKNPEAITE 147
       || ||||| |||||:||| |||||:|||:|||:||| ||||| |||||:|||: ||||: |
Db      61 GKTFVKESLKCIANGITSKVFLTIRRCSSFQKMISEVQEECYSKLDLCSVAQSNPEAMGE 120

Qy      148 VVQLPNHFSNRYYNRLVRSLLLECDEDTVSTIRDSLMEKIGPNMASLFHIL 197
       | |::| | |||: | ::||| ||||| :| |: :: | | || :|
Db      121 VAQVPSQFPNRYYSTLLOSLITCDEDTVEQVRAGLVSRLPEMGVLFOLL 170

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RESULT 9  
US-09-361-736B-9  
; Sequence 9, Application US/09361736B  
; Patent No. 6613877  
; GENERAL INFORMATION:  
; APPLICANT: Human Genome Sciences, Inc.  
; TITLE OF INVENTION: Human Stanniocalcin-Alpha  
; FILE REFERENCE: PF143P1D1  
; CURRENT APPLICATION NUMBER: US/09/361,736B  
; CURRENT FILING DATE: 1999-07-28  
; PRIOR APPLICATION NUMBER: 08/460,529  
; PRIOR FILING DATE: 1995-06-02  
; PRIOR APPLICATION NUMBER: PCT/ US94/13206  
; PRIOR FILING DATE: 1994-11-30

; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 9  
; LENGTH: 170  
; TYPE: PRT  
; ORGANISM: Anguilla australis  
US-09-361-736B-9

Query Match 49.5%; Score 628; DB 4; Length 170;  
Best Local Similarity 66.5%; Pred. No. 1.3e-63;  
Matches 113; Conservative 30; Mismatches 27; Indels 0; Gaps 0;  
  
Qy 28 SPRKSRVAAQNSAEVVRCLNSALQVGCGAFACLENSTCDTGMYDICKSFLYSAAKFDTQ 87  
||| :| :| : ::| ||||| |||||:||||:||||:|||:|||: |||||  
Db 1 SPRTARFSASSPSDVARCLNGALQVGCSAFACLDNSTCNDGMHEICRSFLHGAAKFDTQ 60  
  
Qy 88 GKAFVKESLKCIANGVTSKVFLAIRRCSTFQRMIAEVQEECYSKLNVCASIARKNPEAITE 147  
|| |||||||:|||:||||:|||:|||:|||:|||:|||:|||:|||:|||:  
Db 61 GKTIVKESLKCIANGITSKVFLTIRRCSSFQKMISEVQEECYSKLDLCSVAQSNPEAMGE 120  
  
Qy 148 VVQLPNHFSNRYYNRLVRSILLECDEDTVSTIRDSLMEKIGPNMASLFHIL 197  
| |:|: | |||: | ::||| ||||| :| |: :: | | || :|  
Db 121 VAQVPSQFPNRYYSTLLQSLLTCDDETVEQVRAGLVSRLPEMGVLFQLL 170

#### RESULT 10

US-08-831-132-14

; Sequence 14, Application US/08831132

; Patent No. 6008322

; GENERAL INFORMATION:

; APPLICANT: Kuestner, Rolf E.  
; APPLICANT: Conklin, Darrell C.  
; APPLICANT: Lok, Si  
; APPLICANT: Buddle, Michele  
; APPLICANT: Downey, William  
; TITLE OF INVENTION: STANNIOCALCIN-2  
; NUMBER OF SEQUENCES: 22  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ZymoGenetics, Inc.  
; STREET: 1201 Eastlake Avenue East  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98102

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/831,132  
; FILING DATE:  
; CLASSIFICATION: 424

; ATTORNEY/AGENT INFORMATION:

; NAME: Sawislak, Deborah A.  
; REGISTRATION NUMBER: 37,438  
; REFERENCE/DOCKET NUMBER: 96-01

; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-442-6672  
; TELEFAX: 206-442-6678  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 296 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-831-132-14

Query Match 28.0%; Score 354.5; DB 3; Length 296;  
Best Local Similarity 31.7%; Pred. No. 5.9e-32;  
Matches 85; Conservative 45; Mismatches 109; Indels 29; Gaps 5;

Qy 7 VLLVLVISASATHEAEQNDSVSP-----RKSRAAQNSAEVVRCLNSALQVGCGA 56  
| | || : | : || : | : || : || : || : | | || |  
Db 10 VTLALVF--ATLDPAQGTDSTNPPEGPQDRSSQQKGRSLSLQNTAEIQHCLVNAGDVGCCV 67

Qy 57 FACLENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIAANGVTSKVFLAIRRCST 116  
| | || :: | : | : || : || : | || || : | : | : | : |  
Db 68 FECFENNNSCEIQGLHGICMTFLHNAGKFDAQGKSFIKDALRCKAHALRHKGFCISRKCPA 127

Qy 117 FQRMIAEVQEECYSKLNVCASIARKNPEAITEVVQLPNHFSNRYYNRLVRSILLECDEDTVS 176  
: | : :: | || | : || | : | | | : : : | | || || |  
Db 128 IREMVFQLQRECYLKHDLCSAAQENVGVIVEMIHFKDLLLHEPYVDLVNLLTCGEDVKE 187

Qy 177 TIRDLSMEKIGPNMASLFHIL-----QTDHCAQTH---PRADFNRRRTNEPQKLKV 224  
: | : : : | || : | | || : | | | : | : |  
Db 188 AVTRSVQAQCEQSWGLCSILSFCTSNIQRPPTAAPEHQPLADRAQLSRPHRDTDHHLT 247

Qy 225 LLRNLRLGEEDSPSHIK----RTSHESA 247  
| : || | || | : ||  
Db 248 ANRGAKGERGSKSHPNAHARGRTGGQSA 275

RESULT 11

US-09-416-150-14

; Sequence 14, Application US/09416150  
; Patent No. 6171822

; GENERAL INFORMATION:

; APPLICANT: Kuestner, Rolf E.  
; Conklin, Darrell C.  
; Lok, Si  
; Buddle, Michele  
; Downey, William

; TITLE OF INVENTION: STANNILOCALCIN-2

; NUMBER OF SEQUENCES: 22

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: ZymoGenetics, Inc.  
; STREET: 1201 Eastlake Avenue East  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98102

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/416,150  
FILING DATE: 11-Oct-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/831,132  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Sawislak, Deborah A.  
REGISTRATION NUMBER: 37,438  
REFERENCE/DOCKET NUMBER: 96-01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-442-6672  
TELEFAX: 206-442-6678  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 296 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 14:  
US-09-416-150-14

Query Match 28.0%; Score 354.5; DB 3; Length 296;  
Best Local Similarity 31.7%; Pred. No. 5.9e-32;  
Matches 85; Conservative 45; Mismatches 109; Indels 29; Gaps 5;

Qy 7 VLLVLVISASATHEAEQNDSVSP-----RKSRAAQNSAEVVRCLNSALQVGCGA 56  
| | | | : | : | | : | : | : | : | : | : | : | : |  
Db 10 VTLALVF--ATLDPAQGTDSTNPPEGPQDRSSQQKGRSLSLQNTAEIQHCLVNAGDVGCGV 67

Qy 57 FACLENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIAANGVTSKVFLAIRRCST 116  
| | | | : | : | | : | : | | : | : | : | : | : | : |  
Db 68 FECFENNNSCEIQGLHGICMTFLHNAGKFDAQGKSFIKDALRCKAHALRHKGFCISRKCPA 127

Qy 117 FQRMIAEVQEECYSKLNVCASIARKNPEAITEVVQLPNHFSNRYYNRLVRSILLECDEDTVS 176  
: | : | : | | | | : | : | | | | : | | | | | | | |  
Db 128 IREMVFQLQRECYLKHDLCSAAQENVGVIVEMIHFKDLLLHEPYVDLVNLLTCGEDVKE 187

Qy 177 TIRDSLMEKIGPNMASLFHIL-----QTDHCAQTH---PRADFNRRRTNEPQKLKV 224  
: | : | : | | | | : | | | | | | : | : |  
Db 188 AVTRSVQAQCEQSWGLCSILSFCTSNIQRPPTAAPEHQPLADRAQLSRPHRDTDHHLT 247

Qy 225 LLRNLRLGEEDSPSHIK----RTSHESA 247  
| : | | | | | : |  
Db 248 ANRGAKGERGSKSHPNAHARGRTGGQSA 275

RESULT 12  
US-08-831-132-2  
; Sequence 2, Application US/08831132  
; Patent No. 6008322  
; GENERAL INFORMATION:  
; APPLICANT: Kuestner, Rolf E.

; APPLICANT: Conklin, Darrell C.  
; APPLICANT: Lok, Si  
; APPLICANT: Buddle, Michele  
; APPLICANT: Downey, William  
; TITLE OF INVENTION: STANNIOCALCIN-2  
; NUMBER OF SEQUENCES: 22  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ZymoGenetics, Inc.  
; STREET: 1201 Eastlake Avenue East  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98102  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/831,132  
; FILING DATE:  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sawislak, Deborah A.  
; REGISTRATION NUMBER: 37,438  
; REFERENCE/DOCKET NUMBER: 96-01  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-442-6672  
; TELEFAX: 206-442-6678  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 302 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-831-132-2

Query Match 27.9%; Score 354; DB 3; Length 302;  
Best Local Similarity 32.4%; Pred. No. 6.9e-32;  
Matches 83; Conservative 45; Mismatches 102; Indels 26; Gaps 4;

Qy	9	LVLVIS-----ASATHEAE-QNDSVSPRKSRVAAQNSAEVVRCALNSALQVGCGAFACL	60
	::	:         :    ::     ::	
Db	12	LALVLATFDPARGTDATNPPEGPQDRSSQQKGRLSLQNTAEIQHCLVNAGDVCGVFECF	71
Qy	61	ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM	120
	:: :  ::     :  ::		
Db	72	ENNSCEIRGLHGICMTFLHNAGKFDAQGKSFIKDALKCKAHLRHRFGCISRKCPAIREM	131
Qy	121	IAEVQEECYSKLNVCIAKRNPPEAITEVVQLPNHFSNRYYNRLVRSLLCEDDEDTVSTIRD	180
	:::          :: :		
Db	132	VSQLQRECYLKHDLCIAAQENTRVIVEMIHFKDLLLHEPYVDLVNLLTCGEEVKEAITH	191
Qy	181	SLMEKIGPNMASLFHILO-TDHCAQTHPRADFNRRRTNEPQKL-----	222
	:		
Db	192	SVQVQCEQNWGSLCSILSFCTSAIQKPPTAPPERQPQVDRTKLSRAHHGEAGHHLPEPSS	251

Qy 223 KVLLRNLRGEEDSPSH 238  
: | :|| | ||  
Db 252 RETGRGAKGERGSKSH 267

RESULT 13  
US-09-416-150-2  
; Sequence 2, Application US/09416150  
; Patent No. 6171822  
; GENERAL INFORMATION:  
; APPLICANT: Kuestner, Rolf E.  
; Conklin, Darrell C.  
; Lok, Si  
; Buddle, Michele  
; Downey, William  
; TITLE OF INVENTION: STANNIOLCALCIN-2  
; NUMBER OF SEQUENCES: 22  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ZymoGenetics, Inc.  
; STREET: 1201 Eastlake Avenue East  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98102  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/416,150  
; FILING DATE: 11-Oct-1999  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/831,132  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sawislak, Deborah A.  
; REGISTRATION NUMBER: 37,438  
; REFERENCE/DOCKET NUMBER: 96-01  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-442-6672  
; TELEFAX: 206-442-6678  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 302 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-09-416-150-2

Query Match 27.9%; Score 354; DB 3; Length 302;  
Best Local Similarity 32.4%; Pred. No. 6.9e-32;  
Matches 83; Conservative 45; Mismatches 102; Indels 26; Gaps 4;

Qy 9 LVLVIS-----ASATHEAE-QNDSVSPRKSRAAQN SAEVVRCLNSALQVGCGAFACL 60

Db	12 LALVLATFDPARGTDATNPPEGPQDRSSQQKGRSLQNTAEIQHCLVNAGDVGCGVFECF 71
Qy	61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
Db	72 ENNSCEIRGLHGICMTFLHNAGKFDAQGKSFIDALKCKAHALRHRFGCISRKCPAIREM 131
Qy	121 IAEVQEECYSKLNVCIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLCDEDTVSTIRD 180
Db	132 VSQQLQRECYLKHDLCQAQENTRVIVEMIHFKDLLLHEPYVDLVNLLTCGEEVKEAITH 191
Qy	181 SLMEKIGPNMASLFHILQ-TDHCAQTHPRADFNRRRTNEPQKL----- 222
Db	192 SVQVQCEQNWGSLCSILSFCTSAIQKPPTAPPERQPQVDRTKLSRAHHGEAGHHLPEPSS 251
Qy	223 KVLLRNLRGEEDSPSH 238
Db	252 RETGRGAKGERGSKSH 267

RESULT 14

US-09-193-881-23

; Sequence 23, Application US/09193881A  
; Patent No. 6538119  
; GENERAL INFORMATION:  
; APPLICANT: Patricia Billing-Medel  
; APPLICANT: Maurice Cohen  
; APPLICANT: Tracey L. Colpitts  
; APPLICANT: Paula N. Friedman  
; APPLICANT: Edward N. Granados  
; APPLICANT: Michael R. Klass  
; APPLICANT: John C. Russell  
; APPLICANT: Stephen D. Stroupe  
; TITLE OF INVENTION: Reagents and Methods Useful for Detecting Diseases of the  
; TITLE OF INVENTION: Breast  
; FILE REFERENCE: 6248.US.P1  
; CURRENT APPLICATION NUMBER: US/09/193,881A  
; CURRENT FILING DATE: 1998-11-18  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 23  
; LENGTH: 302  
; TYPE: PRT  
; ORGANISM: Homo sapiens

US-09-193-881-23

Query Match 27.9%; Score 354; DB 4; Length 302;  
Best Local Similarity 32.4%; Pred. No. 6.9e-32;  
Matches 83; Conservative 45; Mismatches 102; Indels 26; Gaps 4;

Qy	9 LVLVIS-----ASATHEAE-QNDSVSPRKSRAAQN SAEVVRLNSALQVGCGAFACL 60
Db	12 LALVLATFDPARGTDATNPPEGPQDRSSQQKGRSLQNTAEIQHCLVNAGDVGCGVFECF 71
Qy	61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
Db	72 ENNSCEIRGLHGICMTFLHNAGKFDAQGKSFIDALKCKAHALRHRFGCISRKCPAIREM 131



Db : | : || | ||  
252 RETGRGAKGERGSKSH 267

Search completed: January 14, 2005, 22:22:14  
Job time : 46 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 14, 2005, 22:04:00 ; Search time 40 Seconds  
(without alignments)  
594.139 Million cell updates/sec

Title: US-10-614-990-2

Perfect score: 1268

Sequence: 1 MLQNSAVLLVLVISASATHE.....NLRGEEDSPSHIKRTSHESA 247

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_79:\*

- 1: pir1:\*
- 2: pir2:\*
- 3: pir3:\*
- 4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result No.	Query					Description
	Score	Match	Length	DB	ID	
1	680.5	53.7	263	2	A54648	stanniocalcin prec
2	662.5	52.2	256	2	I51197	stanniocalcin - co
3	354	27.9	302	2	JE0357	stanniocalcin homo
4	150	11.8	40	2	B60841	teleocalcin - coho
5	149	11.8	40	2	A60841	teleocalcin - sock
6	123	9.7	33	2	S06337	teleocalcin - rain
7	102	8.0	473	2	T04799	hypothetical prote
8	94	7.4	1105	2	T18295	Ap-3 adaptor compl
9	90.5	7.1	289	2	T50776	hypothetical prote
10	90.5	7.1	783	2	T38690	probable regulator
11	89.5	7.1	1126	2	T01491	ubiquitin-protein
12	89	7.0	305	2	T08121	peroxidase (EC 1.1
13	88	6.9	473	2	T45954	hypothetical prote

14	87.5	6.9	1465	2	S45628	DNA-directed DNA p
15	86	6.8	470	2	F86526	Mg++ transporter [
16	86	6.8	470	2	H72097	mg++ transporter (
17	86	6.8	510	2	T45952	hypothetical prote
18	86	6.8	556	2	S51858	probable membrane
19	86	6.8	581	2	S58201	probable membrane
20	83	6.5	250	2	D69215	conserved hypothet
21	83	6.5	250	2	S30584	hypothetical prote
22	83	6.5	365	2	T06693	hypothetical prote
23	83	6.5	1093	2	T50652	AP-3 complex beta3
24	83	6.5	1094	2	T50651	AP3-complex beta-3
25	82.5	6.5	869	2	A88710	protein C43G2.2 [i
26	82.5	6.5	1483	2	S30015	hypothetical prote
27	82.5	6.5	1757	2	T05204	hypothetical prote
28	82.5	6.5	2335	2	T40186	probable phosphati
29	82.5	6.5	2535	2	T04824	hypothetical prote
30	82	6.5	815	2	G72209	conserved hypothet
31	82	6.5	925	2	T01384	hypothetical prote
32	81.5	6.4	463	2	T15416	hypothetical prote
33	81.5	6.4	549	2	F64640	conserved hypothet
34	81.5	6.4	708	1	TFBOL	lactotransferrin p
35	81	6.4	358	2	S76692	hypothetical prote
36	81	6.4	720	2	JC5131	glycosyltransferas
37	81	6.4	1375	2	T18961	FAB1 protein homol
38	81	6.4	4377	2	A55575	ankyrin 3, long sp
39	80	6.3	281	2	H84720	probable endonucle
40	80	6.3	509	1	VGNVPC	major envelope gly
41	80	6.3	509	2	T10395	protein gp64 - Org
42	80	6.3	985	2	T00633	Ca2+-transporting
43	80	6.3	998	2	T52581	Ca2+-transporting
44	80	6.3	1178	2	S54073	probable membrane
45	80	6.3	1188	2	T46608	zinc finger protei

## ALIGNMENTS

### RESULT 1

A54648

stanniocalcin precursor - Australian eel

N;Alternate names: Stannius corpuscle secretory protein

C;Species: *Anguilla australis* (Australian eel)

C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 09-Jul-2004

C;Accession: A54648

R;Butkus, A.; Roche, P.J.; Fernley, R.T.; Haralambidis, J.; Penschow, J.D.; Ryan, G.B.; Trahair, J.F.; Tregear, G.W.; Coghlan, J.P.

Mol. Cell. Endocrinol. 54, 123-133, 1987

A;Title: Purification and cloning of a corpuscles of Stannius protein from *Anguilla australis*.

A;Reference number: A54648; MUID:88083961; PMID:3319739

A;Accession: A54648

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-263 <BUT>

A;Cross-references: UNIPROT:P18301

F;1-17/Domain: signal sequence #status predicted <SIG>

F;18-263/Product: stanniocalcin #status predicted <MAT>

```

Query Match      53.7%;  Score 680.5;  DB 2;  Length 263;
Best Local Similarity 61.4%;  Pred. No. 3.7e-51;
Matches 124;  Conservative 41;  Mismatches 36;  Indels 1;  Gaps 1;

y      1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRAAQNQNSAEVVRCLNSALQVGCGAFACL 60
b          ||: | ::| ||: :| : : :::: :||| :| :| : ::| ||||| ||||||| |||||
1 MLRMSGILTLVL-VTAAYEQDESEPLSPRTARFSASSPSDVARCLNGALQVGCSAFACL 59

y      61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120
b          :|||||:|||||:|||:| ||| ||| ||| ||| |||:||| ||| |||:|||:|||:
60 DNSTCNDGMYEICRSFLHGAAKFDTQGKTFVKESLKCIANGITSKVFLTIRRCSSFQKM 119

y      121 IAEVQEECYSKLNVCIAKRNPAAITEEVVQLPNHFSNRYYNRLVRSILLECDEDTVSTI RD 180
b          |:|||||:|||:|||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:
120 ISEVQEECYSKLDLCSVAQSNPEAMGEVAQVPSQFPNRYYSTLLQSLTCDEDTVEQVRA 179

y      181 SLMEKIGPNMASLFHILQTDHC 202
b          |: ::| | | || :||| |
180 GLVSRLEPEMGVLFQLLQTKAC 201

```

## RESULT 2

151197

### stanniocalcin - coho salmon

C;Species: *Oncorhynchus kisutch* (coho salmon)

C;Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 09-Jul-2004

C;Accession: I51197

R;Wagner, G.F.; Dimattia, G.E.; Davie, J.R.; Copp, D.H.; Friesen, H.G.

Mol. Cell. Endocrinol. 90, 7-15, 1992

A;Title: Molecular cloning and cDNA sequence analysis of coho salmon

### stanniocalcin.

A;Reference number: I51197; MUID:93246046; PMID:1363790

A;Accession: I51197

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A; Residues: 1-256 <WAG>

A;Cross-references: UNIPROT:Q08264; GB:S59519; NID:g299926; PIDN:AAB26419.1;

PID:g299927



R;Wagner, G.F.; Fenwick, J.C.; Park, C.M.; Milliken, C.; Copp, D.H.; Friesen, H.G.  
Gen. Comp. Endocrinol. 72, 237-246, 1988  
A;Title: Comparative biochemistry and physiology of teleocalcin from sockeye and coho salmon.  
A;Reference number: A60841; MUID:89065334; PMID:3197944  
A;Accession: B60841  
A;Molecule type: protein  
A;Residues: 1-40 <WAG>  
A;Cross-references: UNIPROT:Q08264  
C;Comment: This glycoprotein hormone from the corpuscles of Stannius regulates calcium uptake through the gills.  
C;Keywords: disulfide bond; glycoprotein; hormone

Query Match 11.8%; Score 150; DB 2; Length 40;  
Best Local Similarity 66.7%; Pred. No. 2e-06;  
Matches 26; Conservative 6; Mismatches 7; Indels 0; Gaps 0;  
  
Qy 35 AAQNSAEVVRCLNSALQVGCGAFACLENSTCDTDGMYDI 73  
:: : ::| |||| || |||| ||||| |||||:||  
Db 2 SSNSPSDVARCLNGALAVGCGTFACLEXSTCDTDGMHDI 40

RESULT 5  
A60841  
teleocalcin - sockeye salmon (fragment)  
C;Species: Oncorhynchus nerka (sockeye salmon)  
C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 09-Jul-2004  
C;Accession: A60841  
R;Wagner, G.F.; Fenwick, J.C.; Park, C.M.; Milliken, C.; Copp, D.H.; Friesen, H.G.  
Gen. Comp. Endocrinol. 72, 237-246, 1988  
A;Title: Comparative biochemistry and physiology of teleocalcin from sockeye and coho salmon.  
A;Reference number: A60841; MUID:89065334; PMID:3197944  
A;Accession: A60841  
A;Molecule type: protein  
A;Residues: 1-40 <WAG>  
A;Cross-references: UNIPROT:P43649  
C;Comment: This glycoprotein hormone from the corpuscles of Stannius regulates calcium uptake through the gills.  
C;Keywords: disulfide bond; glycoprotein; hormone

Query Match 11.8%; Score 149; DB 2; Length 40;  
Best Local Similarity 76.5%; Pred. No. 2.4e-06;  
Matches 26; Conservative 3; Mismatches 5; Indels 0; Gaps 0;  
  
Qy 40 AEVVRCNSALQVGCGAFACLENSTCDTDGMYDI 73  
::| |||| || |||| ||||| |||||:||  
Db 7 SDVARCLNGALDVGCGTFACLEXSTCDTDGMHDI 40

RESULT 6  
S06337  
teleocalcin - rainbow trout (fragment)  
N;Alternate names: hypocalcin  
C;Species: Oncorhynchus mykiss (rainbow trout)



Db	159 VVDETDLISLKRLLDDFQRKLQELQEKSDRLQKVLEFVSTVHDLCAVRLRLDFLSTVTEVHP 218
Qy	149 -----VQLPNHFSNRYYNRLVRSLLCDEDTVSTIRDSLMEKIGPNMASLFHILQT 199
Db	219 SLDEANGVQTKS-ISNETLARLAKTVLTLKEDKMQRLLKK--LQELATQLTDLWNLMDT 273

RESULT 8

T18295

Ap-3 adaptor complex beta3A chain - mouse

C;Species: Mus musculus (house mouse)

C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004

C;Accession: T18295

R;Feng, L.; Seymour, A.B.; Jiang, S.Y.; To, A.; Peden, A.A.; Novak, E.K.; Zhen, L.; Rusiniak, M.E.; Eicher, E.M.; Robinson, M.S.; Gorin, M.B.; Swank, R.T. Hum. Mol. Genet. 8, 323-330, 1999

A;Title: The beta3A subunit gene (Ap3b1) of the AP-3 adaptor complex is altered in the mouse hypopigmentation mutant pearl, a model for Hermansky-Pudlak syndrome and night blindness.

A;Reference number: Z18864; MUID:99135912; PMID:9931340

A;Accession: T18295

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-1105 <FEN>

A;Cross-references: UNIPROT:Q9Z1T1; EMBL:AF103809; NID:g3885987; PID:g3885988; PIDN:AACT78338.1

A;Experimental source: strain C3H/HeJ

C;Genetics:

A;Gene: Ap3b1

A;Map position: 13

Query Match 7.4%; Score 94; DB 2; Length 1105;  
 Best Local Similarity 21.2%; Pred. No. 6.7;  
 Matches 55; Conservative 40; Mismatches 104; Indels 60; Gaps 11;

Qy	1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRAAQNSAEVVRCLNSALQVGCGAFACL 60
	:  : : : ::   :  :     :     :  :  :
Db	308 LLQSRNAAVVMAVAQLYWH-----ISPKSE--AGVISKSIVRLLRSNREVQYIVLQNI 358

Qy	61 ENSTCDTDGMYD-ICKSFLYSAAKFDTQGKAFVKEISLKCIAANGVTSKVFL----- 109
	: :   ::      :         :
Db	359 ATMSIERKGMFEPYLYKSF-YVRSTDPTMIKTLKLEILTNLANEANISTLLREFQTYVRSQ 417

Qy	110 -----AIRRCSTFQRMIAEVQEECYSKLNVCIAKRNPAAITE---VVQLPNHFS 156
	:   :  :  :     :     ::  :   :    :
Db	418 DKQFAAATIQTIGRCAT--SISEFTETCFNGL-VCLLSNRDEIVVAESVVVIKKLLQMQ 473

Qy	157 NRYYNRLVRSLL-CDEDTVSTIRDSLMEKIGPNMASLFHILQTDHCAQTHPRADFNRR 215
	: :   : :           :        :
Db	474 PAQHGEIIRHMAKFLLSITVPVARASILWILGEN-----CERVPKIA----- 515

Qy	216 TNEPQKLKVLLRNLRGEED 234
	:  :  :  :
Db	516 ---PDVLRKMAKSFTSEDD 531

RESULT 9  
T50776  
hypothetical protein [imported] - Vitis vinifera  
C;Species: Vitis vinifera  
C;Date: 21-Jul-2000 #sequence\_revision 21-Jul-2000 #text\_change 09-Jul-2004  
C;Accession: T50776  
R;Matsumoto, S.; Dry, I.B.; Thomas, M.  
DNA Seq. 8, 109-112, 1997  
A;Title: Nucleotide sequence of grapevine (Vitis vinifera) cDNA similar to SNAP proteins.  
A;Reference number: Z25233  
A;Accession: T50776  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: mRNA  
A;Residues: 1-289 <MAT>  
A;Cross-references: UNIPROT:P93798; EMBL:AB001375; PIDN:BAA19246.1  
A;Experimental source: strain Shiraz

RESULT 10  
T38690  
probable regulatory protein - fission yeast (*Schizosaccharomyces pombe*)  
C;Species: *Schizosaccharomyces pombe*  
C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 16-Aug-2004  
C;Accession: T38690  
R;Brown, D.; Churcher, C.M.; Wood, V.; Barrell, B.G.; Rajandream, M.A.  
submitted to the EMBL Data Library, September 1997  
A;Reference number: Z21805  
A;Accession: T38690  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-783 <BRO>  
A;Cross-references: UNIPROT:O14130; EMBL:Z99568; PIDN:CAB16735.1; GSPDB:GN00066;  
SPDB:SPAC3C7.04  
A;Experimental source: strain 972h-; cosmid c3C7  
C;Genetics:  
A;Gene: SPDB:SPAC3C7.04

A;Map position: 1

C;Superfamily: GAL4 zinc binuclear cluster homology

F;35-71/Domain: GAL4 zinc binuclear cluster homology <GL4>

Query Match 7.1%; Score 90.5; DB 2; Length 783;  
Best Local Similarity 23.3%; Pred. No. 9;  
Matches 56; Conservative 34; Mismatches 87; Indels 63; Gaps 12;

Qy 10 VLVISASATHEAEQNDSVSPRKSrv-----AAQNSAEVVRCLNSALQVGCGAF----- 57  
Db 535 IIIMSRPVLLHKMKNAKNSPRVDRINEDCILAARHLISLVHLLQNHSQLSCYSFFDYNYT 594

Qy 58 -----ACLENSTCDTDGMYDICKSFLYSAAKFTQGKAFVKESLKCI----- 99  
Db 595 FSSALVVLLHCV-TEPCEED---DIAMQYAYSALDYMAEGNEAAKNCARVIRLFDAHLKG 650

Qy 100 ----ANGVTSKV-FLAIRRCSTFQRMIAEVQ-----EECYSKLNVCASIARKRNPEAITEVV 149  
Db 651 ARSDGNGNTSQSGFMA-----WQRWIAEVSAKDEPEKLMSPYNKSIGGGRNSNSLTPNA 704

Qy 150 QLPNHFSNRYYNR-----LVRSLLECDEDTVSTIRDSLMEKIGPNMA---SLFHILQTD 200  
Db 705 NLGADVS--FFPTDDTSFLLDHSKLDDLEKFASTLDPI--KTPDLANDSSLNWANTD 760

RESULT 11

T01491

ubiquitin-protein ligase homolog F1707.15 - *Arabidopsis thaliana*

C;Species: *Arabidopsis thaliana* (mouse-ear cress)

C;Date: 12-Feb-1999 #sequence\_revision 12-Feb-1999 #text\_change 09-Jul-2004

C;Accession: T01491

R;Vysotskaia, V.S.; Schwartz, J.R.; Toriumi, M.; Yu, G.; Kwan, A.; Oji, O.; Liu, S.; Li, J.; Araujo, R.; Au, M.; Brendel, V.; Buehler, E.; Conway, A.B.; Conway, A.R.; Dewar, K.; Feng, J.; Kim, C.; Kurtz, D.; Li, Y.; Palm, C.J.; Shinn, P.; Sun, H.; Davis, R.W.; Ecker, J.R.; Federspiel, N.A.; Theologis, A.  
submitted to the EMBL Data Library, June 1998

A;Description: *Arabidopsis thaliana* chromosome 1 BAC F1707 sequence.

A;Reference number: Z14334

A;Accession: T01491

A;Status: translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-1126 <VYS>

A;Cross-references: UNIPROT:064605; EMBL:AC003671; NID:g2833627; PID:g3176690; GSPDB:GN00059; ATSP:F1707.15

A;Experimental source: cultivar Columbia

C;Genetics:

A;Gene: ATSP:F1707.15

A;Map position: 1

A;Introns: 118/3; 224/3; 292/1; 373/3; 457/2; 826/3; 875/3; 902/3; 1057/3; 1093/2

F;756-1120/Domain: ubiquitin-protein ligase homology <UBI>

Query Match 7.1%; Score 89.5; DB 2; Length 1126;  
Best Local Similarity 22.1%; Pred. No. 17;  
Matches 46; Conservative 39; Mismatches 76; Indels 47; Gaps 8;

Qy 14 SASATHEAEQNDSVSPRKSrvAAQNSAEVVRCLNSALQVGCGAFACLENSTCD----- 66



Db	177 LSGAHTIGQARCTTFRQRI-----YNDTNIDPAFATTRRGNCQAGAGANLAPLDGTP	229
Qy	153 NHFSNRYYNRLV--RSLLCDEDVTST-IRDSDLMEKIGPNMASLFHILQTDHCAQ----	204
Db	230 TQFDNRYYQDLVARRGLLHSDQELFNNGTQDALVRTYSNNAAT---FATDFAAMVRMG	285
Qy	205 -----THPRADFNRRRTN 217	
Db	286 NISPLTGTNGEIRFNCRPN 305	

RESULT 13

T45954

hypothetical protein F7J8.120 - *Arabidopsis thaliana*

C;Species: *Arabidopsis thaliana* (mouse-ear cress)

C;Date: 04-Feb-2000 #sequence\_revision 04-Feb-2000 #text\_change 09-Jul-2004

C;Accession: T45954

R;Bevan, M.; Zimmermann, W.; Grueneisen, A.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; Lemcke, K.; Mayer, K.F.X.

submitted to the Protein Sequence Database, January 2000

A;Reference number: Z23018

A;Accession: T45954

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-473 <BEV>

A;Cross-references: UNIPROT:Q9LFC2; EMBL:AL137189

A;Experimental source: cultivar Columbia; BAC clone F7J8

C;Genetics:

A;Map position: 5

A;Introns: 29/1; 428/3

A;Note: F7J8.120

C;Superfamily: *Arabidopsis thaliana* hypothetical protein F7J8.130

Query Match 6.9%; Score 88; DB 2; Length 473;  
 Best Local Similarity 22.6%; Pred. No. 8.1;  
 Matches 54; Conservative 42; Mismatches 103; Indels 40; Gaps 13;

Qy	27 VSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACLEN--STCD---TDGMYDICKS-FLY	79
Db	16 IDEEKNKVVLAEAGTIVRLLAKHRKSDPVTIGCLRNLYTSVVDMELEDDFETDACKQMLLY	75

Qy	80 SAAKFDTQGKAF----VKESLKCIAANGVTSKVFLAIRRCSTFQRMIAE---VQEEC--	128
Db	76 PKNIREAQYRNFKLNIDTNESLKCFG---CRFFSICRMCSNFNTSLCKCGKLMNEEISF	131

Qy	129 --YSKLNVCIAKRNPEA--ITEVVQLPNHFSNRYYNRLVRSLLCDEDVTSTIRDSIME	184
Db	132 LEYEENDVEGVFMRDKSSFIITDDLRLTDDST---SSLLQTLKDLGCADVSKLREQVLD	187

Qy	185 KIGPNMASLFHILQTDHCAQTH--PRAD--FNRRRTNEPQKLKVLLRNLRGEEKDPSHI	239
Db	188 -IG----LKEVMTLMQCVFTSNTPLTDAFLKNQSSNTVRKIYRKLSDDKGDEAEPDKV	240

RESULT 14

S45628

DNA-directed DNA polymerase (EC 2.7.7.7) alpha 180K chain - mouse  
N;Alternate names: DNA polymerase alpha/DNA primase complex 180K chain  
C;Species: Mus musculus (house mouse)  
C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 09-Jul-2004  
C;Accession: S45628; A46642  
R;Stadlbauer, F.; Brueckner, A.; Rehfuss, C.; Eckerskorn, C.; Lottspeich, F.;  
Foerster, V.; Tseng, B.Y.; Nasheuer, H.P.  
Eur. J. Biochem. 222, 781-793, 1994  
A;Title: DNA replication in vitro by recombinant DNA-polymerase-alpha-primase.  
A;Reference number: S45628; MUID:94298818; PMID:8026492  
A;Accession: S45628  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-1465 <STA>  
A;Cross-references: UNIPROT:P33609; EMBL:D17384; NID:g397829; PIDN:BAA04202.1;  
PID:g442471  
R;Miyazawa, H.; Izumi, M.; Tada, S.; Takada, R.; Masutani, M.; Ui, M.; Hanaoka, F.  
J. Biol. Chem. 268, 8111-8122, 1993  
A;Title: Molecular cloning of the cDNAs for the four subunits of mouse DNA  
polymerase alpha-primase complex and their gene expression during cell  
proliferation and the cell cycle.  
A;Reference number: A46642; MUID:93216788; PMID:8463324  
A;Accession: A46642  
A;Status: preliminary.  
A;Molecule type: mRNA; protein  
A;Residues: 4-1465 <MIY>  
A;Experimental source: FM3A cells  
A;Note: sequence extracted from NCBI backbone (NCBIN:129146, NCBIP:129147)  
C;Superfamily: DNA polymerase  
C;Keywords: DNA binding; nucleotidyltransferase; nucleus

Query Match 6.9%; Score 87.5; DB 2; Length 1465;  
Best Local Similarity 20.7%; Pred. No. 34;  
Matches 34; Conservative 32; Mismatches 55; Indels 43; Gaps 7;

Qy 6 AVLLVLVISASAT-----HEAEQNDSVSPRKSRSVAAQNSAEVVRLNSALQVGCGAFA 58  
| ||: | : :| |: |: ||::: :: : : | |  
Db 1236 AVLIALWLGLDSTQFRVHQYHKDEENDALLGGPAQLTDEEKYK-----DCEKFK 1284

Qy 59 CLENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVT-----SKVFLAIR 112  
| | | | : :|| :: : | : : : | : | : | : : ||  
Db 1285 CLCPS-CGTENIYD---NVFEGSGLDMEPSLYRCNSVDCKVSPLETFMVQLSNKLMDIR 1339

Qy 113 RCSTFQRMIAEVQEECYSKLNVCIAKRNPAAITEVVQLPNHFS 156  
| | :: | : | : : : || ||  
Db 1340 RCI-----KKYYDGWLIC---EEPTCCSRLRRPLHFS 1369

RESULT 15  
F86526  
Mg++ transporter [imported] - Chlamydophila pneumoniae (strain J138)  
C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae  
C;Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004  
C;Accession: F86526  
R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.;  
Shiba, T.; Ishii, K.; Hattori, M.; Kuhara, S.; Nakazawa, T.

Nucleic Acids Res. 28, 2311-2314, 2000

A;Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.

A;Reference number: A86491; MUID:20330349; PMID:10871362

A;Accession: F86526

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-470 <STO>

A;Cross-references: UNIPROT:Q9Z8Q2; GB:BA000008; NID:g8978660; PIDN:BAA98496.1;  
GSPDB:GN00142

A;Experimental source: strain J138

C;Genetics:

A;Gene: mgtE

C;Superfamily: magnesium transport protein mgtE

Query Match 6.8%; Score 86; DB 2; Length 470;  
Best Local Similarity 22.9%; Pred. No. 12;  
Matches 47; Conservative 33; Mismatches 61; Indels 64; Gaps 13;

Qy 56 AFACLENSTCDTD-GMYDICK-----SFLYSAAKFDTQGKAFVKESLKCIANGVTSK 106  
|| || || :|: | |: : : :| : ::| || |: |

Db 19 AFTCL-----STDIHSHDLSKIVIEYNPIDLAYAVSCLPSESRAILYKNLSCI---TAK 69

Qy 107 VFLAIR-----RCSTFQRMIAEVQEECYSKLNVCASIARKNP--EAITEVVQLPNHFSNRY 159  
| | | :|: | | ||: :| | |: :| :| :|

Db 70 VAFIINTDSASRWAIFRRL-----SDSEVCALIEQMPPDEAVWVLDDIP---DRR 116

Qy 160 YNRLVRSLLECDEDTVSTIRDSLMEKIGPNMA-----SLFHIL-----QTDHCAQTHP 207  
| |:: : | | || :| | | | | | | | :|

Db 117 YRRILELI---DSKKALKIRD--LQKHGRNTAGRLMTNEFFAFLMETTVKDVSACIRSNP 171

Qy 208 RADFNRRRTNEPQKLKVLLRNLRGE 232  
| | | :| :|

Db 172 GIDLTR-----LVFVLDFKGE 187

Search completed: January 14, 2005, 22:21:27

Job time : 52 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 14, 2005, 22:18:31 ; Search time 149 Seconds  
(without alignments)  
598.916 Million cell updates/sec

Title: US-10-614-990-2  
Perfect score: 1268  
Sequence: 1 MLQNSAVLLVLVISASATHE.....NLRGEEDSPSHIKRTSHESA 247

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1608061 seqs, 361289386 residues

Total number of hits satisfying chosen parameters: 1608061

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_AA:\*

1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*

2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*

3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*

4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep:\*

5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*

6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep:\*

7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*

8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*

9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep:\*

10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep:\*

11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep:\*

12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:\*

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16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep:\*

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18: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep:\*

19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*

20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1268	100.0	247	9	US-09-840-989A-2	Sequence 2, Appli
2	1268	100.0	247	9	US-09-361-736-10	Sequence 10, Appl
3	1268	100.0	247	13	US-10-116-051-2	Sequence 2, Appli
4	1268	100.0	247	14	US-10-177-293-441	Sequence 441, App
5	1268	100.0	247	14	US-10-418-226-10	Sequence 10, Appl
6	1268	100.0	247	14	US-10-465-572-18	Sequence 18, Appl
7	1268	100.0	247	15	US-10-372-683-41	Sequence 41, Appl
8	1268	100.0	247	17	US-10-614-990-2	Sequence 2, Appli
9	1268	100.0	247	17	US-10-723-860-4202	Sequence 4202, Ap
10	937	73.9	276	9	US-09-925-300-1426	Sequence 1426, Ap
11	662.5	52.2	256	9	US-09-840-989A-3	Sequence 3, Appli
12	662.5	52.2	256	17	US-10-614-990-3	Sequence 3, Appli
13	660.5	52.1	204	13	US-10-116-051-10	Sequence 10, Appl
14	628	49.5	170	9	US-09-361-736-9	Sequence 9, Appli
15	628	49.5	170	14	US-10-418-226-9	Sequence 9, Appli
16	358	28.2	70	9	US-09-864-761-37770	Sequence 37770, A
17	354	27.9	302	9	US-09-193-881-23	Sequence 23, Appl
18	354	27.9	302	14	US-10-177-293-443	Sequence 443, App
19	354	27.9	302	14	US-10-338-395-23	Sequence 23, Appl
20	354	27.9	302	14	US-10-418-226-12	Sequence 12, Appl
21	354	27.9	302	14	US-10-364-889-4	Sequence 4, Appli
22	354	27.9	302	14	US-10-295-027-100	Sequence 100, App
23	354	27.9	302	15	US-10-173-999-80	Sequence 80, Appl
24	354	27.9	302	15	US-10-058-270A-22	Sequence 22, Appl
25	354	27.9	302	17	US-10-789-378-74	Sequence 74, Appl
26	351.5	27.7	251	14	US-10-418-226-2	Sequence 2, Appli
27	333.5	26.3	251	9	US-09-361-736-2	Sequence 2, Appli
28	303	23.9	118	13	US-10-116-051-9	Sequence 9, Appli
29	95.5	7.5	299	15	US-10-282-122A-49895	Sequence 49895, A
30	94.5	7.5	415	17	US-10-425-115-320042	Sequence 320042,
31	92	7.3	1010	17	US-10-425-115-312927	Sequence 312927,
32	91	7.2	901	10	US-09-828-062-8	Sequence 8, Appli
33	91	7.2	901	16	US-10-768-511-8	Sequence 8, Appli
34	90.5	7.1	783	15	US-10-149-310-96	Sequence 96, Appl
35	90	7.1	281	11	US-09-973-278-172	Sequence 172, App
36	90	7.1	281	11	US-09-973-278-277	Sequence 277, App
37	90	7.1	331	15	US-10-264-049-2324	Sequence 2324, Ap
38	89.5	7.1	622	16	US-10-437-963-161551	Sequence 161551,
39	89.5	7.1	1123	15	US-10-282-122A-70581	Sequence 70581, A
40	89.5	7.1	10203	16	US-10-661-809-23	Sequence 23, Appl
41	89	7.0	201	17	US-10-425-115-320050	Sequence 320050,
42	89	7.0	431	17	US-10-425-115-285165	Sequence 285165,
43	86	6.8	401	15	US-10-425-114-63193	Sequence 63193, A
44	86	6.8	470	15	US-10-282-122A-54827	Sequence 54827, A
45	86	6.8	500	15	US-10-289-762-299	Sequence 299, App

#### ALIGNMENTS

RESULT 1  
 US-09-840-989A-2  
 ; Sequence 2, Application US/09840989A  
 ; Patent No. US20020042372A1

; GENERAL INFORMATION:  
; APPLICANT: Olsen et al.  
; TITLE OF INVENTION: Stanniocalcin Polynucleotides, Polypeptides, and Methods  
Based Thereon  
; FILE REFERENCE: PF108P2  
; CURRENT APPLICATION NUMBER: US/09/840,989A  
; CURRENT FILING DATE: 2001-04-25  
; PRIOR APPLICATION NUMBER: PCT/US00/29432  
; PRIOR FILING DATE: 2000-10-26  
; PRIOR APPLICATION NUMBER: US 60/161,740  
; PRIOR FILING DATE: 1999-10-27  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 247  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-840-989A-2

Query Match 100.0%; Score 1268; DB 9; Length 247;  
Best Local Similarity 100.0%; Pred. No. 1e-120;  
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRAAQNQSAEVVRCLNSALQVGCGAFACL 60  
Db 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRAAQNQSAEVVRCLNSALQVGCGAFACL 60

Qy 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120  
Db 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120

Qy 121 IAEVQEECYSKLNVCIAKRNP EAITEVVQLPNHFSNRYNRLVRSLL ECDEDTVSTIRD 180  
Db 121 IAEVQEECYSKLNVCIAKRNP EAITEVVQLPNHFSNRYNRLVRSLL ECDEDTVSTIRD 180

Qy 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240  
Db 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240

Qy 241 RTSHESA 247  
Db 241 RTSHESA 247

RESULT 2  
US-09-361-736-10  
; Sequence 10, Application US/09361736  
; Patent No. US20020102634A1  
; GENERAL INFORMATION:  
; APPLICANT: OLSEN, ET AL.  
; TITLE OF INVENTION: Human Stanniocalcin-alpha  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,  
; ADDRESSEE: CECCHI, STEWART & OLSTEIN  
; STREET: 6 BECKER FARM ROAD  
; CITY: ROSELAND

;  
; STATE: NEW JERSEY  
; COUNTRY: USA  
; ZIP: 07068  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 INCH DISKETTE  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: WORD PERFECT 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/361,736  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/460,529  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MULLINS, J.G.  
; REGISTRATION NUMBER: 33,073  
; REFERENCE/DOCKET NUMBER: 325800-334 (PF143)  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201-994-1700  
; TELEFAX: 201-994-1744  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 247 AMINO ACIDS  
; TYPE: AMINO ACID  
; STRANDEDNESS:  
; TOPOLOGY: LINEAR  
; MOLECULE TYPE: PROTEIN  
US-09-361-736-10

Query Match 100.0%; Score 1268; DB 9; Length 247;  
Best Local Similarity 100.0%; Pred. No. 1e-120;  
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCALQVGCGAFACL 60  
Db 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCALQVGCGAFACL 60

Qy 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120  
Db 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120

Qy 121 IAEVQEECYSKLNVCIAKRNP EAITEVVQLPNHFSNRYYNRLVRSILLECDEDTVSTIRD 180  
Db 121 IAEVQEECYSKLNVCIAKRNP EAITEVVQLPNHFSNRYYNRLVRSILLECDEDTVSTIRD 180

Qy 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240  
Db 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240

Qy 241 RTSHESA 247  
Db 241 RTSHESA 247

RESULT 3

US-10-116-051-2

; Sequence 2, Application US/10116051  
; Publication No. US20020146791A1  
; GENERAL INFORMATION:  
; APPLICANT: Olsen et al.  
; TITLE OF INVENTION: CORPUSCLES OF STANNIUS PROTEIN, STANNIOPROTEIN  
; FILE REFERENCE: PF108P1D1C1  
; CURRENT APPLICATION NUMBER: US/10/116,051  
; CURRENT FILING DATE: 2002-04-05  
; PRIOR APPLICATION NUMBER: 09/312,610  
; PRIOR FILING DATE: 1999-05-17  
; PRIOR APPLICATION NUMBER: 08/431,117  
; PRIOR FILING DATE: 1995-04-28  
; PRIOR APPLICATION NUMBER: 08/208,005  
; PRIOR FILING DATE: 1994-03-08  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 247  
; TYPE: PRT  
; ORGANISM: Homo sapiens

US-10-116-051-2

Query Match 100.0%; Score 1268; DB 13; Length 247;  
Best Local Similarity 100.0%; Pred. No. 1e-120;  
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MLQNSAVLLVLVISASATHEAEQNDVS PRKS RVA A QNSAEV VRCLNS ALQVGCGA FACL	60
Db	1	MLQNSAVLLVLVISASATHEAEQNDVS PRKS RVA A QNSAEV VRCLNS ALQVGCGA FACL	60
Qy	61	ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM	120
Db	61	ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM	120
Qy	121	IAEVQEECYSKLNVC SIAKR NPEAITEVVQLPNHFSN RYYNRLVRS LLECDDED TVSTIRD	180
Db	121	IAEVQEECYSKLNVC SIAKR NPEAITEVVQLPNHFSN RYYNRLVRS LLECDDED TVSTIRD	180
Qy	181	SLMEKIGPNMASLFH ILO TDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK	240
Db	181	SLMEKIGPNMASLFH ILO TDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK	240
Qy	241	RTSHESA 247	
Db	241	RTSHESA 247	

RESULT 4

US-10-177-293-441  
; Sequence 441, Application US/10177293  
; Publication No. US20030124128A1  
; GENERAL INFORMATION:  
; APPLICANT: Lillie, James  
; APPLICANT: Glatt, Karen  
; APPLICANT: Zhao, Xumei  
; APPLICANT: Gannavarpu, Manjula

; APPLICANT: Kamatkar, Shubhangi  
; APPLICANT: Mertens, Maureen  
; APPLICANT: Myer, Vic  
; APPLICANT: Wang, Youzhen  
; APPLICANT: Xu, Yongyao  
; APPLICANT: Hoersch, Sebastian  
; APPLICANT: Monahan, John  
; APPLICANT: Meyers, Rachel E.  
; APPLICANT: Bast Jr., Robert C.  
; APPLICANT: Hortobagyi, Gabriel N.  
; APPLICANT: Pusztai, Lajos  
; APPLICANT: Meric, Funda  
; APPLICANT: Sahin, Aysegul  
; APPLICANT: Mills, Gordon B.  
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION,  
ASSESSMENT,  
; TITLE OF INVENTION: PREVENTION, AND THERAPY OF BREAST CANCER  
; FILE REFERENCE: MRI-038  
; CURRENT APPLICATION NUMBER: US/10/177,293  
; CURRENT FILING DATE: 2002-06-21  
; PRIOR APPLICATION NUMBER: US 60/299,887  
; PRIOR FILING DATE: 2001-06-21  
; PRIOR APPLICATION NUMBER: US 60/301,572  
; PRIOR FILING DATE: 2001-06-27  
; PRIOR APPLICATION NUMBER: US 60/306,501  
; PRIOR FILING DATE: 2001-07-18  
; PRIOR APPLICATION NUMBER: US 60/325,002  
; PRIOR FILING DATE: 2001-09-25  
; PRIOR APPLICATION NUMBER: US 60/362,585  
; PRIOR FILING DATE: 2002-03-05  
; PRIOR APPLICATION NUMBER: US 60/xxx,xxx  
; PRIOR FILING DATE: 2002-05-14  
; NUMBER OF SEQ ID NOS: 506  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 441  
; LENGTH: 247  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-177-293-441

Query Match 100.0%; Score 1268; DB 14; Length 247;  
Best Local Similarity 100.0%; Pred. No. 1e-120;  
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRAAQNSAEVVRCLNSALQVGCGAFACL 60  
Db 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRAAQNSAEVVRCLNSALQVGCGAFACL 60

Qy 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFRAIRRCSTFQRM 120  
Db 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFRAIRRCSTFQRM 120

Qy 121 IAEVQEECYSKLNVCASIARKNPEAITEVVQLPNHFSNRYYNRLVRSLLCEDDEDTVSTIRD 180  
Db 121 IAEVQEECYSKLNVCASIARKNPEAITEVVQLPNHFSNRYYNRLVRSLLCEDDEDTVSTIRD 180

Qy 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEDSPSHIK 240

Db 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240  
|||  
Qy 241 RTSHESA 247  
|||  
Db 241 RTSHESA 247

RESULT 5

US-10-418-226-10

; Sequence 10, Application US/10418226  
; Publication No. US20030181663A1  
; GENERAL INFORMATION:  
; APPLICANT: Human Genome Sciences, Inc.  
; TITLE OF INVENTION: Human Stanniocalcin-Alpha  
; FILE REFERENCE: PF143P1D2  
; CURRENT APPLICATION NUMBER: US/10/418,226  
; CURRENT FILING DATE: 2003-04-18  
; PRIOR APPLICATION NUMBER: 09/361,736  
; PRIOR FILING DATE: 1999-07-28  
; PRIOR APPLICATION NUMBER: 08/460,529  
; PRIOR FILING DATE: 1995-06-02  
; PRIOR APPLICATION NUMBER: PCT/ US94/13206  
; PRIOR FILING DATE: 1994-11-30  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 10  
; LENGTH: 247  
; TYPE: PRT  
; ORGANISM: human

US-10-418-226-10

Query Match 100.0%; Score 1268; DB 14; Length 247;  
Best Local Similarity 100.0%; Pred. No. 1e-120;  
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60  
|||  
Db 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60  
Qy 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVLAIIRRCSTFQRM 120  
|||  
Db 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVLAIIRRCSTFQRM 120  
Qy 121 IAEVQEECYSKLNVCIAKRNP EAITEVVQLPNHFSNRYYNRLVRSLL ECDEDTVSTIRD 180  
|||  
Db 121 IAEVQEECYSKLNVCIAKRNP EAITEVVQLPNHFSNRYYNRLVRSLL ECDEDTVSTIRD 180  
Qy 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240  
|||  
Db 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240  
Qy 241 RTSHESA 247  
|||  
Db 241 RTSHESA 247

RESULT 6  
US-10-465-572-18  
; Sequence 18, Application US/10465572  
; Publication No. US20030207840A1  
; GENERAL INFORMATION:  
; APPLICANT: Riggins, Gregory  
; APPLICANT: Lal, Anita  
; TITLE OF INVENTION: GENES INDUCED BY HYPOXIA  
; FILE REFERENCE: 000250.00012  
; CURRENT APPLICATION NUMBER: US/10/465,572  
; CURRENT FILING DATE: 2003-06-20  
; PRIOR APPLICATION NUMBER: US/10/201,642  
; PRIOR FILING DATE: 2002-07-24  
; PRIOR APPLICATION NUMBER: 60/307,600  
; PRIOR FILING DATE: 2001-07-26  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 18  
; LENGTH: 247  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-465-572-18

Query Match 100.0%; Score 1268; DB 14; Length 247;  
Best Local Similarity 100.0%; Pred. No. 1e-120;  
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRAAQNQSAEVVRCLNSALQVGCGAFACL 60  
|||  
Db 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRAAQNQSAEVVRCLNSALQVGCGAFACL 60  
  
Qy 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120  
|||  
Db 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120  
  
Qy 121 IAEVQEECYSKLNVCIAKRNP EAITEVVQLPNHFSNRYYNRLVRSLL ECDEDTVSTIRD 180  
|||  
Db 121 IAEVQEECYSKLNVCIAKRNP EAITEVVQLPNHFSNRYYNRLVRSLL ECDEDTVSTIRD 180  
  
Qy 181 SLMEKIGPNMASLFHILOTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240  
|||  
Db 181 SLMEKIGPNMASLFHILOTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240  
  
Qy 241 RTSHESA 247  
|||  
Db 241 RTSHESA 247

RESULT 7  
US-10-372-683-41  
; Sequence 41, Application US/10372683  
; Publication No. US20040009171A1  
; GENERAL INFORMATION:  
; APPLICANT: GERRITSEN, MARY E.  
; APPLICANT: PEALE JR., FRANKLIN V.  
; APPLICANT: WU, THOMAS D.  
; TITLE OF INVENTION: METHODS FOR THE TREATMENT OF CARCINOMA

; FILE REFERENCE: P1928R1P1  
; CURRENT APPLICATION NUMBER: US/10/372,683  
; CURRENT FILING DATE: 2003-02-21  
; PRIOR APPLICATION NUMBER: US 10/271,690  
; PRIOR FILING DATE: 2002-10-16  
; PRIOR APPLICATION NUMBER: US 60/344,534  
; PRIOR FILING DATE: 2001-10-18  
; NUMBER OF SEQ ID NOS: 49  
; SEQ ID NO 41  
; LENGTH: 247  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-10-372-683-41

Query Match 100.0%; Score 1268; DB 15; Length 247;  
Best Local Similarity 100.0%; Pred. No. 1e-120;  
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCNSALQVGCGAFACL	60
Db	1	MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCNSALQVGCGAFACL	60
Qy	61	ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM	120
Db	61	ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM	120
Qy	121	IAEVQEECYSKLNVCISIARKNPEAITEVVQLPNHFSNRYYNRLVRSILLECDEDTVSTIRD	180
Db	121	IAEVQEECYSKLNVCISIARKNPEAITEVVQLPNHFSNRYYNRLVRSILLECDEDTVSTIRD	180
Qy	181	SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK	240
Db	181	SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK	240
Qy	241	RTSHESA 247	
Db	241	RTSHESA 247	

#### RESULT 8

US-10-614-990-2  
; Sequence 2, Application US/10614990  
; Publication No. US20040198658A1  
; GENERAL INFORMATION:  
; APPLICANT: Olsen et al.  
; TITLE OF INVENTION: Stanniocalcin Polynucleotides, Polypeptides, and Methods  
Based Thereon  
; FILE REFERENCE: PF108P2  
; CURRENT APPLICATION NUMBER: US/10/614,990  
; CURRENT FILING DATE: 2003-07-09  
; PRIOR APPLICATION NUMBER: US/09/840,989A  
; PRIOR FILING DATE: 2001-04-25  
; PRIOR APPLICATION NUMBER: PCT/US00/29432  
; PRIOR FILING DATE: 2000-10-26  
; PRIOR APPLICATION NUMBER: US 60/161,740  
; PRIOR FILING DATE: 1999-10-27  
; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 247  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-614-990-2

Query Match 100.0%; Score 1268; DB 17; Length 247;  
Best Local Similarity 100.0%; Pred. No. 1e-120;  
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60  
Db 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRVAAQNSAEVVRCLNSALQVGCGAFACL 60

Qy 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120  
Db 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120

Qy 121 IAEVQEECYSKLNVCASIARKNPEAITEVVQLPNHFSNRYYNRLVRSLLCEDDEDTVSTIRD 180  
Db 121 IAEVQEECYSKLNVCASIARKNPEAITEVVQLPNHFSNRYYNRLVRSLLCEDDEDTVSTIRD 180

Qy 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240  
Db 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240

Qy 241 RTSHESA 247  
Db 241 RTSHESA 247

RESULT 9  
US-10-723-860-4202  
; Sequence 4202, Application US/10723860  
; Publication No. US20040253606A1  
; GENERAL INFORMATION:  
; APPLICANT: Aziz, Natasha  
; APPLICANT: Ginsburg, Wendy M.  
; APPLICANT: Zlotnik, Albert  
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions  
&  
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators  
; FILE REFERENCE: 05882.0193.NPUS01  
; CURRENT APPLICATION NUMBER: US/10/723,860  
; CURRENT FILING DATE: 2003-11-26  
; PRIOR APPLICATION NUMBER: 60/429,739  
; PRIOR FILING DATE: 2002-11-26  
; NUMBER OF SEQ ID NOS: 8393  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 4202  
; LENGTH: 247  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-723-860-4202

Query Match 100.0%; Score 1268; DB 17; Length 247;

Best Local Similarity 100.0%; Pred. No. 1e-120;  
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRAAQNQSAEVVRCLNSALQVGCGAFACL 60  
Db 1 MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRAAQNQSAEVVRCLNSALQVGCGAFACL 60  
Qy 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120  
Db 61 ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM 120  
Qy 121 IAEVQEECYSKLNVCASIARKNPEAITEVVQLPNHFSNRYYNRLVRSILLECDEDTVSTIRD 180  
Db 121 IAEVQEECYSKLNVCASIARKNPEAITEVVQLPNHFSNRYYNRLVRSILLECDEDTVSTIRD 180  
Qy 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240  
Db 181 SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK 240  
Qy 241 RTSHESA 247  
Db 241 RTSHESA 247

RESULT 10

US-09-925-300-1426

; Sequence 1426, Application US/09925300

; Patent No. US20020151681A1

; GENERAL INFORMATION:

; APPLICANT: Craig Rosen,

; APPLICANT: Steve Ruben

; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

; FILE REFERENCE: PA101

; CURRENT APPLICATION NUMBER: US/09/925,300

; CURRENT FILING DATE: 2001-08-10

; PRIOR APPLICATION NUMBER: PCT/US00/05988

; PRIOR FILING DATE: 2000-03-08

; PRIOR APPLICATION NUMBER: 60/124,270

; PRIOR FILING DATE: 1999-03-12

; NUMBER OF SEQ ID NOS: 1890

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 1426

; LENGTH: 276

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: SITE

; LOCATION: (43)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

; NAME/KEY: SITE

; LOCATION: (273)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

; NAME/KEY: SITE

; LOCATION: (275)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

US-09-925-300-1426

Query Match 73.9%; Score 937; DB 9; Length 276;  
 Best Local Similarity 99.5%; Pred. No. 6.8e-87;  
 Matches 185; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRAAQNQSAEVVRCLNSALQVGCGAFACL	60
Db	89	MLQNSAVLLVLVISASATHEAEQNDSVSPRKSRAAQNQSAEVVRCLNSALQVGCGAFACL	148
Qy	61	ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM	120
Db	149	ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRM	208
Qy	121	IAEVQEECYSKLNVCIAKRNPPEAITEVVQLPNHFSNRYYNRLVRSLLCEDEDTVSTIRD	180
Db	209	IAEVQEECYSKLNVCIAKRNPPEAITEVVQLPNHFSNRYYNRLVRSLLCEDEDTVSTIRD	268
Qy	181	SLMEKI 186	
Db	269	SLMEXI 274	

RESULT 11

US-09-840-989A-3

; Sequence 3, Application US/09840989A  
 ; Patent No. US20020042372A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Olsen et al.  
 ; TITLE OF INVENTION: Stanniocalcin Polynucleotides, Polypeptides, and Methods  
 Based Thereon  
 ; FILE REFERENCE: PF108P2  
 ; CURRENT APPLICATION NUMBER: US/09/840,989A  
 ; CURRENT FILING DATE: 2001-04-25  
 ; PRIOR APPLICATION NUMBER: PCT/US00/29432  
 ; PRIOR FILING DATE: 2000-10-26  
 ; PRIOR APPLICATION NUMBER: US 60/161,740  
 ; PRIOR FILING DATE: 1999-10-27  
 ; NUMBER OF SEQ ID NOS: 12  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 3  
 ; LENGTH: 256  
 ; TYPE: PRT  
 ; ORGANISM: Oncorhynchus kisutch

US-09-840-989A-3

Query Match 52.2%; Score 662.5; DB 9; Length 256;  
 Best Local Similarity 53.4%; Pred. No. 6.1e-59;  
 Matches 125; Conservative 46; Mismatches 54; Indels 9; Gaps 4;

Qy	11	LVISASATHEAEQNDSVSPRKSRAAQNQSAEVVRCLNSALQVGCGAFACLENSTCDTG	70
	: :   : : :  ::  : : :		
Db	12	LVLGTAATFDTDPEEA-SPRRARFSSNSPSDVARCLNGALAVGCGTFACLENSTCDTG	70
Qy	71	YDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRMIAEVQEECYS	130
	:   :  :     :         :                     :		
Db	71	HDICQLFFHTAATFNTQGKTFVKESLRCIANGVTSKVFTQIRRCGVFQRMISEVQEECYS	130
Qy	131	KLNVCIAKRNPPEAITEVVQLPNHFSNRYYNRLVRSLLCEDEDTVSTIRD	190
	MEKIGPNM		



; Publication No. US20020146791A1  
; GENERAL INFORMATION:  
; APPLICANT: Olsen et al.  
; TITLE OF INVENTION: CORPUSCLES OF STANNIUS PROTEIN, STANNIocalcIN  
; FILE REFERENCE: PF108P1D1C1  
; CURRENT APPLICATION NUMBER: US/10/116,051  
; CURRENT FILING DATE: 2002-04-05  
; PRIOR APPLICATION NUMBER: 09/312,610  
; PRIOR FILING DATE: 1999-05-17  
; PRIOR APPLICATION NUMBER: 08/431,117  
; PRIOR FILING DATE: 1995-04-28  
; PRIOR APPLICATION NUMBER: 08/208,005  
; PRIOR FILING DATE: 1994-03-08  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 10  
; LENGTH: 204  
; TYPE: PRT  
; ORGANISM: Oncorhynchus kisutch  
US-10-116-051-10

Query Match 52.1%; Score 660.5; DB 13; Length 204;  
Best Local Similarity 60.8%; Pred. No. 7.1e-59;  
Matches 118; Conservative 38; Mismatches 37; Indels 1; Gaps 1;

Qy 11 LVISASATHEAEQNDSVSPRKSRAAQNSAEVVRCLNSALQVGGAFACLENSTCDTDGM 70  
||: :|| : : :: ||:::| :: : ::| |||| || |||| |||||||||||||  
Db 12 LVLGTAATFDTDPEEA-SPRRARFSSNSPSDVARCLNGALAVGCGTFACLENSTCDTDGM 70

Qy 71 YDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFQRMIAEVQEECYS 130  
:|||: | :||| | :||| | :|||:| :|||:| :|||:| :|||:| :|||:| :|||:|  
Db 71 HDICQLFFHTAATFNTQGKTFVKESLRCIANGVTSKVQTIIRRCGVFQRMISEVQEECYS 130

Qy 131 KLNVCSIAKRNPEAITEVVQLPNHFSNRYNRLVRSILLECDEDTVSTIRDSLMEKIGPNM 190  
:||:| :|: | :||| | :|||:| | :|||:| :|||:| :|||:| :| | :|||:|  
Db 131 RLDICGVARSNPEAIGEVVQVPAHFPNRYYSTLLQSLACDEETVAVVRAGLVARLGPDM 190

Qy 191 ASLFHILQTDHCAQ 204  
:|| :|| | | |  
Db 191 ETLFQOLLQNKHCPQ 204

RESULT 14  
US-09-361-736-9  
; Sequence 9, Application US/09361736  
; Patent No. US20020102634A1  
; GENERAL INFORMATION:  
; APPLICANT: OLSEN, ET AL.  
; TITLE OF INVENTION: Human StanniocalcIN-alpha  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,  
; ADDRESSEE: CECCHI, STEWART & OLSTEIN  
; STREET: 6 BECKER FARM ROAD  
; CITY: ROSELAND  
; STATE: NEW JERSEY  
; COUNTRY: USA

ZIP: 07068  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 INCH DISKETTE  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WORD PERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/361,736  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/460,529  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: MULLINS, J.G.  
REGISTRATION NUMBER: 33,073  
REFERENCE/DOCKET NUMBER: 325800-334 (PF143)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-994-1700  
TELEFAX: 201-994-1744  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 170 AMINO ACIDS  
TYPE: AMINO ACID  
STRANDEDNESS:  
TOPOLOGY: LINEAR  
MOLECULE TYPE: PROTEIN

US-09-361-736-9

Query Match 49.5%; Score 628; DB 9; Length 170;  
Best Local Similarity 66.5%; Pred. No. 1.e-55;  
Matches 113; Conservative 30; Mismatches 27; Indels 0; Gaps 0;

Qy 88 GKAFVKESLKCIANGVTSKVFLAIRRCSTFQRMIAEVQEECYSKLNVCIAKRNPEAITE 147

Db 61 GKT FVKE SLK CIANG IT SKVFLT IRRCSS FQKM I SEVQ EECYS KLDLCS VQA QSNPEAMGE 120

Db 121 VAQVPSQFPNRYYSTLLQSLLTCDEDTVEQVRAGLVSRLPEPMGVLFQLL 170

### RESULT 15

US-10-418-226-9

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; TYPE: PRT  
; ORGANISM: Anguilla australis  
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Query Match 49.5%; Score 628; DB 14; Length 170;  
Best Local Similarity 66.5%; Pred. No. 1.1e-55;  
Matches 113; Conservative 30; Mismatches 27; Indels 0; Gaps 0;

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Qy	88	GKAFVKESLKCIANGVTSKVFLAIRRCSTFQRMIAEVQEECYSKLNVCASIAGRNPAAITE	147
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Qy	148	VVQLPNHFSNRYYNRLVRSLLCDEDTVSTIRDSLMEKIGPNMASLFHIL	197
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